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| (54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE | | | |
| (57) Abstract Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided. | | | |

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATETM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1.

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate. Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| ATCAAATCTG | AGGGTTGTCT | GGAGGACTTC | AATAACACCTC | CCCCCATAGT | GAATCAGCTT | 120 |
| CCAGGGGGTC | CAGTCCCTCT | CCTTAACCTCA | TCCCCATCCC | ATGCCAAAGG | AAGACCCCTCC | 180 |
| CTCCCTGGCT | CACAGCCTTC | TCTAGGCTTC | CCAGTGCCTC | CAGGACAGAG | TGGGTTATGT | 240 |
| TTTCAGCTCC | ATCCTTGTCTG | TGAGTGTCTG | GTGCGTTGTG | CCTCCAGCTT | CTGCTCAGTG | 300 |
| CTTCATGGAC | AGTGTCCAGC | ACATGTCACT | CTCCACTCTC | TCAGTGTGGA | TCCACTAGTT | 360 |
| CTAGAGCCGC | CGGCCACCGCG | GTGGAGCTCC | AGCTTTGTGTT | CCCTTTAGTG | AGGGTTAATT | 420 |
| GCCCGCTTGG | CGTAATCATG | GTCATAACTG | TTTCCGTGTG | GAAATTGTTA | TCCGCTCACA | 480 |
| ATTCACACACA | ACATACGAGC | CGGAAGCATA | AAGTGTAAAG | CCTGGGGTGC | CTAATGAGTG | 540 |
| ANCTAACTCA | CATTAATTGC | GTTGCGCTCA | CTGNCCGCTT | TCCAGTCNGG | AAAACGTGCG | 600 |
| TGCCAGCTGC | ATTAATGAAT | CGGCCAACGC | NCGGGGAAAAA | GCGGTITGCG | TTT'GGGGGGC | 660 |
| TCTTCCGCTT | CTCGCTCACT | NANTCCTGCG | CTCGGTCTNT | CGGCTGCGGG | GAACGGTATC | 720 |
| ACTCCTAAA | GGNGGTATTA | CGGTTATCCN | NAAATCNGGG | GATACCCNGG | AAAAAANTTT | 780 |
| ACAAAAGGG | CANCAAAGGG | CNGAAACGTA | AAAA | | | 814 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ACAGAAATGT | TGGATGGTGG | AGCACCTTTC | TATACGACTT | ACAGGACAGC | AGATGGGAA | 60 |
| TTCATGGCTG | TTGGAGCAAT | AGAACCCAG | TTCTACGAGC | TGCTGATCAA | AGGACTTTGGA | 120 |
| CTAAAGTCTG | ATGAACTTCC | CAATCAGATG | AGCATGGATG | ATTGGCCAGA | AATGAAGAAG | 180 |
| AAGTTTGCAG | ATGTATTTC | AAAGAAGACG | AAGGCAGAGT | GGTGTCAAAT | CTTTGACGGC | 240 |
| ACAGATGCCT | GTGTGACTCC | GGTTCTGACT | TTTGAGGAGG | TTGTTCATCA | TGATCACAAC | 300 |
| AAGGAACGGG | GCTCGTTAT | CACCAGTGAG | GAGCAGGACG | TGAGCCCCCG | CCCTGCACCT | 360 |
| CTGCTGTTAA | ACACCCAGC | CATCCCTCT | TTCAAAAGGG | ATCCACTAGT | TCTAGAAGCG | 420 |
| GCCGCCACCG | CGGTGGAGCT | CCAGCTTTG | TTCCCTTTAG | TGAGGGTTAA | TTGCGCGCTT | 480 |
| GGCGTAATCA | TGGTCATAGC | TGTTCCCTGT | GTGAAATTGT | TATCCGCTCA | CAATTCCCCC | 540 |
| AACATACGAG | CCGGAACATA | AAGTGTAAAG | CCTGGGGTGC | CTAATGANTG | AGCTAACTCN | 600 |
| CATTAATTGC | GTTGCGCTCA | CTGCCGCTT | TCCAGTCGGG | AAAACGTGCG | TGCCACTGCN | 660 |
| TTANTGAATC | NGCCACCCCC | CGGGAAAAGG | CGGTTCTNT | TTGGGCTCT | TCCGCTTTCC | 720 |
| TCGCTCATTG | ATCCTNGNC | CCGGTCTTCG | GCTGCGGNGA | ACGGTTCACT | CCTCAAAGGC | 780 |
| GGTNTNCCGG | TTATCCCCAA | ACNGGGATA | CCCNGA | | | 816 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|--------------|------------|-------------|-----|
| CTTTTGAAAG | AAGGGATGGC | TGGGGTGT | TAAACAGCAGAG | GTGCAGGGCG | GGGGCTCACC | 50 |
| TCCTGCTCCT | CACTGGTGAT | AAACGAGCCC | CGTTCTTGT | TGTGATCATG | ATGAACAAACC | 120 |

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| TCCTCAAAAG | TCAGAACCGG | AGTCACACAG | GCATCTGTGC | CGTCAAAGAT | TTGACACCAC | 180 |
| TCTGCCCTCG | TCTTCTTTGC | AAATACATCT | GCAAACCTCT | TCTTCATTTTC | TGGCCAATCA | 240 |
| TCCATGCTCA | TCTGATTGGG | AAGTCATCA | GACTTTAGTC | CANNTCTTT | GATCAGCAGC | 300 |
| TCGTAGAACT | GGGGTTCTAT | TGCTCCAACA | GCCATGAATT | CCCCATCTGC | TGTCCTGTAA | 360 |
| GTCGTATAGA | AAGGTGCTCC | ACCATCCAAC | ATGTTCTGTG | CTCGAGGGGG | GGCCCGGTAC | 420 |
| CCAATTGCC | CTATANTGAG | TCTGATTACG | CGCGCTCACT | GGCCGTCGTT | TTACAACGTC | 480 |
| GTGACTGGGA | AAACCCCTGGG | CGTTACCAAC | TTAATCGCT | TGCAGCACAT | CCCCCTTCG | 540 |
| CCAGCTGGGC | GTAATANCGA | AAAGGCCGC | ACCGATCGCC | CTTCCAACAG | TTGCGCACCT | 600 |
| GAATGGGNA | ATGGGACCCC | CCTGTTACCG | CGCATTNAAC | CCCCGCNNGG | TTTNGTTGTT | 660 |
| ACCCCCACNT | NNACCGCTTA | CACTTTGCCA | GCGCCTTANC | GCCCGCTCCC | TTTCNCCTTT | 720 |
| CTTCCCTTCC | TTTCNCNNCN | CTTTCCCCCG | GGGTTTCCCC | CNTCAAACCC | CNA | 773 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| CCTCCTGAGT | CCTACTGACC | TGTGCTTCT | GGTGTGGAGT | CCAGGGCTGC | TAGGAAAAGG | 60 |
| AATGGCAGA | CACAGGTGTA | TGCCAATGTT | TCTGAAATGG | GTATAATTTC | GTCCCTCTCCT | 120 |
| TCGGAACACT | GGCTGTCTCT | GAAGACTTCT | CGCTCAGTTT | CAGTGAGGAC | ACACACAAAG | 180 |
| ACGTGGTGA | CCATGTTGTT | TGTGGGGTGC | AGAGATGGGA | GGGGTGGGGC | CCACCCCTGGA | 240 |
| AGAGTGGACA | GTGACACAAG | GTGGACACTC | TCTACAGATC | ACTGAGGATA | AGCTGGAGCC | 300 |
| ACAATGCATG | AGGCACACAC | ACAGCAAGGA | TGACNCTGTA | AACATAGCCC | ACGCTGTCCT | 360 |
| GNGGGCACTG | GGAAGCCTAN | ATNAGGCCGT | GAGCANAAG | AAGGGGAGGA | TCCACTAGTT | 420 |
| CTANAGCGGC | CGCCACCGCG | GTGGANCTCC | ANCTTTTGTT | CCCTTTAGTG | AGGGTTAATT | 480 |
| GCGCGTTGG | CNTAATCATG | GTCATANCTN | TTTCCTGTGT | GAAATTGTTA | TCCGCTCACA | 540 |
| ATTCCACACA | ACATACGANC | CGGAAACATA | AANTGTAAAC | CTGGGGTGCC | TAATGANTGA | 600 |
| CTAACTCACA | TTAATTGCGT | TGCGCTACT | GCCCCGTTTC | CAATCNGGAA | ACCTGTCTTG | 660 |
| CCNCTTGCAT | TNATGAATCN | GCCAACCCCC | GGGGAAAAGC | GTGGCGTTT | TGGCGCTCT | 720 |
| TCCGCTTCCCT | CNCTCANTTA | NTCCCTNCNC | TCGGTCATTC | CGGCTGCNGC | AAACCGGTTC | 780 |
| ACCNCTCCA | AAGGGGTAT | TCCGGTTTCC | CCNAATCCGG | GGANANCC | | 828 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTACTGA | TAGATGGAAT | TTATTAAGCT | TTTCACATGT | GATAGCACAT | 60 |
| AGTTTTAATT | GCATCCAAAG | TACTAACAAA | AACTCTAGCA | ATCAAGAATG | GCAGCATGTT | 120 |
| ATTTTATAAC | AATCAACACC | TGTGGCTTTT | AAAATTTGGT | TTTCATAAGA | TAATTTATAC | 180 |
| TGAAGTAAAT | CTAGCCATGC | TTTTAAAAAA | TGCTTTAGGT | CACTCCAAGC | TTGGCAGTTA | 240 |

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|------------|-----|
| ACATTTGGCA | TAAACAATAA | AAAAACAATC | ACAATTAA | AAATAACAAA | TACAACATTG | 300 |
| TAGGCCATAA | TCATATACAG | TATAAGGAAA | AGGTGGTAGT | GTTGAGTAAG | CAGTTATTAG | 360 |
| AATAGAATAC | CTTGGCCTCT | ATGCAAATAT | GTCTAGACAC | TTTGATTACAC | TCAGCCCTGA | 420 |
| CATTCAGTTT | TCAAAGTAGG | AGACAGGTTTC | TACAGTATCA | TTTTACAGTT | TCCAACACAT | 480 |
| TGAAAACAAG | TAGAAAATGA | TGAGTTGATT | TTTATTAAATG | CATTACATCC | TCAAGAGTTA | 540 |
| TCACCAACCC | CTCAGTTATA | AAAAATTTC | AGTTTATATT | AGTCATATAA | CTTGGTGTGC | 600 |
| TTATTTTAAA | TTAGTGCTAA | ATGGATTAAG | TGAAGACAAAC | AATGGTCCCC | TAATGTGATT | 660 |
| GATAITGGTC | ATTTTTACCA | GCTTCTAAAT | CTNAACTTTTC | AGGCTTTGA | ACTGGAACAT | 720 |
| TGNATNACAG | TGTTCCANAG | TTNCAACCTA | CTGGAACATT | ACAGTGTGCT | TGATTCAAAA | 780 |
| TGTTATTTTG | TTAAAAAATTA | AATTAAACC | TGGTGGAAAAA | ATAATTGAA | ATNA | 834 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | AAGACCTCA | TCAATAGATG | GAGACATACA | GAAATAGTCA | 60 |
| AACCACATCT | ACAAAATGCC | AGTATCAGGC | GGCGGCTTCG | AAGCCAAAGT | GATGTTTGGA | 120 |
| TGTAAAGTGA | AATATTAGTT | GGCGGATGAA | GCAGATAGTG | AGGAAAGTTG | AGCCAATAAT | 180 |
| GACGTGAAGT | CCGTGGAAGC | CTGTGGCTAC | AAAAAATGTT | GAGCCGTAGA | TGCCGTCGGA | 240 |
| AATGGTGAAG | GGAGACTCGA | AGTACTCTGA | GGCTTGTAGG | AGGGTAAAAT | AGAGACCCAG | 300 |
| TAAAATTGTA | ATAAGCAGTG | CTTGAATTAT | TTGGTTTCGG | TTGTTTCTA | TTAGACTATG | 360 |
| GTGAGCTCAG | GTGATTGATA | CTCCTGATGC | GAGTAATACG | GATGTGTTA | GGAGTGGGAC | 420 |
| TTCTAGGGGA | TTTAGCGGGG | TGATGCCTGT | TGGGGGCCAG | TGCCCTCCTA | GTTGGGGGGT | 480 |
| AGGGGCTAGG | CTGGAGTGGT | AAAAGGCTCA | AAAAAATCCT | GCGAAGAAAA | AAACTTCTGA | 540 |
| GGTAATAAAAT | AGGATTATCC | CGTATCGAAG | GCCTTTTGG | ACAGGTGGTG | TGTGGTGGCC | 600 |
| TTGGTATGTG | CTTTCTCGTG | TTACATCGCG | CCATCATTGG | TATATGTTA | GTGTGTTGGG | 660 |
| TTANTANGC | CTANTATGAA | GAACCTTTGG | ANTGGAATTA | AATCAATNGC | TTGGCCGGAA | 720 |
| GTCATTANGA | NGGCTNAAAA | GGCCCTGTCA | NGGGTCTGGG | CTNGTTTTA | CCCNACCCAT | 780 |
| GGAATNCNCC | CCCCGGACNA | NTGNATCCCT | ATTCTTAA | | | 818 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TGGCTCTAGA | GGGGTAGAG | GGGGTGCAT | AGGGTAAATA | 60 |
| CGGGCCCTAT | TTCAAAGATT | TTTAGGGAA | TTAATTCTAG | GACGATGGGT | ATGAAACTGT | 120 |
| GGTTTGCTCC | ACAGATTCA | GAGCATTGAC | CGTAGTATAC | CCCCGGTCGT | GTAGCGGTGA | 180 |
| AACTGGTTTG | GTTTAGACGT | CCGGAATTG | CATCTGTTT | TAAGCTAAT | GTGGGGACAG | 240 |
| CTCATGAGTG | CAAGACGTCT | TGTGATGAA | TTATTATACN | AATGGGGCCT | TCAATCGGGA | 300 |

| | | |
|---|-----------------------|-----|
| GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC | TGGTTCTAGG AATAATGGGG | 360 |
| GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT | GTTCTCTAG GTTCAATACC | 420 |
| ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT | TGAACTCGTC TGTATGTAA | 480 |
| AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA | TNAATGGCGG GCANGATATT | 540 |
| TCAAACNGTC TCTANTCCT GAAACGTCTG AAATGTTAAT | AANAATTAAN TTTNGTTATT | 600 |
| GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT | ANGAAAANTA ATNNTAANGG | 660 |
| CNTTATCNTN AAAGGTNATA ACCNCTCTA TNATCCCACC | CAATNGNATT CCCCACNCNN | 720 |
| ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG | TGNANNCCNC CTTTGTTCC | 780 |
| CTTNANTGAN GGTTATTCCNC CCCTNGCNTT ATCANC | | 817 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | |
|--|------------------------|-----|
| CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC | TGCTAACGTG GGAATCGGTG | 60 |
| CATAAGGAGA ACTTTCTGCT GGCACCGCGCT AGGGACAAGC | GGGAGAGCGA CTCCGAGCGT | 120 |
| CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC | AGCTGGGACA CATCCGCGAG | 180 |
| TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC | AGTGTAGCCG CGTCCTGGGG | 240 |
| TGGGTGGCCG ANGCCTGANC CGCTCTGCCT TGCTGCCCTC | ANGTGGGCCG CCACCCCCCTG | 300 |
| ACCTGCGCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT | CAAGGANAAC CCCCACANGG | 360 |
| GGATTTGCT CCTANANTAA GGCTCATCTG GGCTCGGCC | CCCCCACCTG GTTGGCCTTG | 420 |
| TCTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG | GACCACCTT NGGGAGTGT | 480 |
| CTCCCTAACAA CCACANNATG CCCGCTCCT CCCGAAACC | ANTCCCANCC TGNGAAGGAT | 540 |
| CAAGNCCTGN ATCCACTNNT NCTANAACCG GGCNCCNCCG | CNGTGGAACCC CNCCCTNTGT | 600 |
| TCCCTTTCNT TNAGGGTTAA TNNGCCTTG GCCTTNCCAN | NGTCCTNCNC NTTTCCNNT | 660 |
| GTTNAAATTG TTANGCNCC NCCNNTCCN CNNCNNCNAN | CCCGACCCNN ANNTNNNANN | 720 |
| NCCCTGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT | TGCNTTNGGG NNCNNTGCC | 780 |
| CTTTCCCTCT NGGGANNNCG | | 799 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | |
|---|-----------------------|-----|
| ACGCCCTTGAT CCTCCCCAGGC TGGGACTGGT TCTGGGAGGA | GCCGGGCATG CTGTGGTTTG | 60 |
| TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA | GATGGACATG GGGCTCACCT | 120 |
| CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCCACAT | GATCCTTAAT CTATGAGCAA | 180 |
| AATCCCTGT GGGGGCTTCT CCTTGAAAGTC CGCCANCAGG | GCTCAGTCTT TGGACCCANG | 240 |
| CAGGTGATGG GGTTGTNGNC CAACTGGGG CCNCAACGCA | AAANGGCNCA GGGCCTCNGN | 300 |
| CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCCNC | TCCACCACTT TCATGCGCTG | 360 |

| | |
|--|-----|
| TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCNAC TCCANCTTCT NGGACGTGCG | 420 |
| CTACATACGC CCGGANTCNC NCTCCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATT | 480 |
| CNCCNTANTG CACCNATTCC CACNTTNNC AGNTTTCCNC NNCGNGCTTC CTTNTAAAAG | 540 |
| GGTTGANCCC CGGAAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACNT CCCCCCTNATA | 600 |
| GCTGAANTCC CCATNACCCN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT | 660 |
| GGGAANANCC CTCGNCCNTN CCCCCNTTAA TCCCNCCTTG CNANGNNCNT CCCCCNNNTCC | 720 |
| NCCCNNTNG GCNTNTNANN CNAAAAAGGC CCNNNNANCAA TCTCCTNNCN CCTCANTTCG | 780 |
| CCANCCCTCG AAATCGGCCN C | 801 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|---|-----|
| CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC | 60 |
| ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC | 120 |
| AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCTGCCCCA | 180 |
| AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCCTGC | 240 |
| CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGTGGA GGCAGTGGCC | 300 |
| TGCTCCCACC TCCACCCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCCTCC GTACGTGTGG | 360 |
| TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCGG GGGCATCTGC CTGGACCTCG | 420 |
| CCATCCTGGA TAGTGTCTCC TGCTGTCCTA NGTGGCCCA TCCCTGTTA TGGGCTCCAT | 480 |
| TGTCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCCGCAGGCC TGGGTCTGGT | 540 |
| CCCATTAACT TTGCTACACA GGTANTATTT GACAAGAACG ANTTGGCCAA ATACTCAGCG | 600 |
| TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGTCC AACTCCCCGC | 660 |
| TCCTGTTAAC CCCATGGGGC TGCGGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT | 720 |
| GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG | 780 |
| GGNGTTCCC | 789 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|--|-----|
| CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC | 60 |
| TTTGTAAAT AAATAAGTTA AATATTTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG | 120 |
| ACCAACAGGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC | 180 |
| TGTGGGCTGA GGGGACCTGG TTCTTGTGTC TTGCCCCCTCA GGACTCTTCC CCTACAAATA | 240 |
| ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTCATCC TAGAAACTCC CATGCAAGAG | 300 |
| CTACATTAAA CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT | 360 |
| TATTCAGCTC CCAAAACCC TTCTCTAGGT GTGTCTAAC TAGGAGGCTA GCTGTTAAC | 420 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGAGCCTGG | GTAATCCACC | TGCAGAGTCC | CCGCATTCCA | GTGCATGGAA | CCCTTCTGGC | 480 |
| CTCCCTGTAT | AAGTCCAGAC | TGAAACCCCC | TTGGAAGGNC | TCCAGTCAGG | CAGCCCTANA | 540 |
| AACTGGGAA | AAAAGAAAAG | GACGCCCCAN | CCCCCAGCTG | TGCANCTACG | CACCTCAACA | 600 |
| GCACAGGGTG | GCAGCAAAAA | AACCACTTTA | CTTTGGCACA | AACAAAAACT | NGGGGGGGCA | 660 |
| ACCCCGGCAC | CCCNANGGGG | GTAAACAGGA | ANCNGGGNAA | CNTGGAACCC | AATTNAGGCA | 720 |
| GGCCCNCCAC | CCCNAATNTT | GCTGGGAAAT | TTTCCTCCC | CTAAATTNTT | TC | 772 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|------------|-----|
| GCCCCAATT | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCCCTC | TACTTTTGG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT | GTCATTGCAA | CAGAATGGGG | GAAAGGCACT | TTCTCTTTG | 180 |
| AAGTANGGTG | AGTCCTCAAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGGTGT | TCCACACTTG | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GGAAGTGCCTC | AGCCATTGTG | GTGTACACCA | AGGCGACCAC | 360 |
| AGCAGCTGCN | ACCTCAGCAA | TGAAGATGAN | GAGGANGATG | AAGAAGAACG | TCNCGAGGGC | 420 |
| ACACTTGCTC | TCAGTCTTAN | CACCATANCA | CCCCNTGAAA | ACCAANANCA | AAGACCACNA | 480 |
| CNCCGGCTGC | GATGAAGAAA | TNACCCNCG | TTGACAAACT | TGCATGGCAC | TGGGANCCAC | 540 |
| AGTGGCCNA | AAAATCTTCA | AAAAGGATGC | CCCATCNATT | GACCCCCCAA | ATGCCCACTG | 600 |
| CCAACAGGGG | CTGCCCCACN | CNCNNAACGA | TGANCCNATT | GNACAAGATC | TNCNTGGTCT | 660 |
| TNATNAACNT | GAACCCGTGCN | TNGTGGCTCC | TGTTCAAGGNC | CNNGGCCTGA | CTTCTNAANN | 720 |
| AANGAACTCN | GAAGNCCCCA | CNGGANANNC | G | | | 751 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAGCCAGGCG | TCCCTCTGCC | TGCCCACTCA | GTGCAACAC | CCGGGAGCTG | TTTGTCCCTT | 60 |
| TGTGGANCT | CAGCAGTNCC | CTCTTTAGA | ACTCANTGCC | AAGANCCCTG | AAACAGGAGCC | 120 |
| ACCATGCACT | GCTTCAGCTT | CATTAAGACC | ATGATGATCC | TCTTCATTT | GCTCATCTTT | 180 |
| CTGTGTGGTG | CAGCCCTGTT | GGCAGTGGGC | ATCTGGGTGT | CAATCGATGG | GGCATCCTTT | 240 |
| CTGAAGATCT | TGGGGCCACT | GTCGTCCAGT | GCCATGCAGT | TTGTCAACGT | GGGCTACTTC | 300 |
| CTCATCGCAG | CCGGCGTTGT | GGTCTTAGCT | CTAGGTTTC | TGGGCTGCTA | TGGTGCTAAG | 360 |
| ACTGAGAGCA | AGTGTGCCCT | CGTGACGTT | TTCTTCATCC | TCCTCCTCAT | CTTCATTGCT | 420 |
| GAGGTTGCAA | TGCTGTGGTC | GCCTTGGGTG | ACACCACAA | GGCTGAGCAC | TTCTGTACGT | 480 |
| TGCTGGTAAT | GCCTGCCATC | AANAAAAGAT | TATGGGTTCC | CAGGAANACT | TCACTCAAGT | 540 |
| GTTGGAACAC | CACCATGAAA | GGGCTCAAGT | GCTGTGGCTT | CNNCCAACTA | TACGGATT | 600 |

| | |
|--|-----|
| GAAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTCCCCC ATTTCTGTTG CAATTGACAA | 660 |
| ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAAACCC AAANGGGTCC CCAACCANAA | 720 |
| ATTNAAGGG | 729 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | |
|---|-----|
| TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG | 60 |
| TGTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGAGAG TCCTGTGTCT | 120 |
| GGCAGGTCCA CGCAGTGCCTC TTTGTCACTG GGGAAATGGA TGCGCTGGAG CTCGTCAAAG | 180 |
| CCACTCGTGT ATTTTTCACA GGCAGCCTCG TCCGACGCGT CGGGGCAGTT GGGGGTGTCT | 240 |
| TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGGCTGA | 300 |
| CANGTGCCAG AGCACACTGG ATGGCGCTT TCCATGNAN GGGCCCTGNG GGAAAGTCCC | 360 |
| TGANCCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACACA CCCCAGACAGG CTAGAATGGA | 420 |
| ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCCCNNTAA ACAAACTCTT | 480 |
| GCANATCTGC TCCGNGGGGG TCNTANTACC ANC GTGGGAA AAGAACCCCA GGCGNGGAAC | 540 |
| CAANCTTGTG TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA | 600 |
| CTGTNNNACT TTAGNCCNTG GTCCTCNTGG GTTGNNTTG AACCTAATCN CCNTCAACT | 660 |
| GGGACAAGGT AAANTNGCCNT CTTTNAATT CCCNANCNTN CCCCCTGGTT TGGGGTTTTN | 720 |
| CNCNCTCCTA CCCCAGAAAAN NCCGTGTTCC CCCCCAACTA GGGGCNAAA CCNNTTNTTC | 780 |
| CACAACCCTN CCCCACCCAC GGTTNGGGTNG | 816 |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | |
|--|-----|
| CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG | 60 |
| ATGTGGAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA | 120 |
| AAGACCCAAA CCAGGTGGAA CTGTGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA | 180 |
| CAGTGACTAG CTCAGACCCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA | 240 |
| CCAAGCAGAC AGAAGACTAC TGCCTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT | 300 |
| TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTTCGTT TATGGAGGCT | 360 |
| GCTTGGGCAA CAAGAACAAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTCNGGGTG | 420 |
| TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCT | 480 |
| CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA | 540 |
| NCAATGGCTG CTGCATCNAC ANTTTCCCTNG AATTGTGACA ACACCCCCCA NTGCCCCCAA | 600 |
| CCCTCCCAAC AAAGCTTCCC TGTTAAAAA TACNCCANTT GGCTTTNAC AACACNCCCGG | 660 |
| CNCCTCCNTT TTCCCCNNTN AACAAAGGGC NCTNGCNTTT GAACTGCCN AACCCNGGAA | 720 |

| | |
|---|-----|
| TCTNCCNNGG AAAAANTNCC CCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCC | 780 |
| CCC | 783 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | |
|---|-----|
| GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTGGAT GTCATACAAA | 60 |
| AGCTGATTGA AGCAACCCCTC TACTTTTGG TCGTGAGCCT TTTGCTTGTT GCAGGTTTCA | 120 |
| TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACT GTTCTCTTTG | 180 |
| AAGTAGGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC | 240 |
| ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTT CTTGATGGCA | 300 |
| GGCACTACCA GCAACGTCAG GAAGTGTCA GCCATTGTGG TGTACACCAA GGCACCA | 360 |
| GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA | 420 |
| CACTTGCTCT CCGCTTCTAGC ACCATAGCAG CCCANGAAAC CAAGAGAAA GACCACAACG | 480 |
| CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGGCCACT GGACGACAGT | 540 |
| TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATGATTG AACACCCANA TGCCCAC | 600 |
| CNACAGGGCT GCNCCNCNCN GAAAGAATGA GCCATTGAAG AAGGATCN | 660 |
| TGAAC | 720 |
| AAAGAACNGC NTNAGCCCCC CCAAANGANA AAACACCCCCC GGGTGTG | 780 |
| GGCCAAGGAN CCCTGCCCCN G | 801 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|--|-----|
| GTGAGAGCCA GGCGTCCCTC TGCCTGCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT | 60 |
| CCTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG | 120 |
| AGCCACCATG CAGTGCTTC GCTTCATTAA GACCATGATG ATCCTCTTC ATTGCTCAT | 180 |
| CTTCTGTGT GGTGCAGCCC TGTTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC | 240 |
| CTTCTGAAG ATCTCGGGC CACTGTCGTC CAGTGCCATG CAGTTGTCA ACGTGGGCTA | 300 |
| CTTCCTCATC GCAGCCGGCG TTGTGGTCTT TGCTCTTGGT TTCCCTGGCT GCTATGGTGC | 360 |
| TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT | 420 |
| TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCAATTCC | 480 |
| GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAAGGAA AAATTCACTC | 540 |
| AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATACCG | 600 |
| GAATTTTGAA AGANTCNCCC TACTTCAAA AAAAAANANT TGCCCTTNCC CCCNTTCTGT | 660 |
| TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNAAA | 720 |
| CAAAAAAANT NNAAGGGTTN | 740 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | | | | | | |
|------------|-------------|-------------|------------|-------------|------------|-----|
| CCGCTGGTTG | CGCTGGTCCA | GNGNAGCCAC | GAAGCACGTC | AGCATAACACA | GCCTCAATCA | 60 |
| CAAGGTCTTC | CAGCTGCCGC | ACATTACGCA | GGGCAAGAGC | CTCCAGCAAC | ACTGCATATG | 120 |
| GGATACACTT | TACTTTAGCA | GCCAGGGTGA | CAACTGAGAG | GTGTCGAAGC | TTATTCTTCT | 180 |
| GAGCCTCTGT | TAGTGGAGGA | AGATTCCGGG | CTTCAGCTAA | GTAGTCAGCG | TATGTCCCCT | 240 |
| AAGCAAACAC | TGTGAGCAGC | CGGAAGGTAG | AGGCAAAGTC | ACTCTCAGCC | AGCTCTCTAA | 300 |
| CATTGGGCAT | GTCCAGCAGT | TCTCCAAACA | CGTAGACACC | AGNGGCCTCC | AGCACCTGAT | 360 |
| GGATGAGTGT | GGCCAGCGCT | GCCCCCTTGG | CCGACTTGGC | TAGGAGCAGA | AATTGCTCCT | 420 |
| GGTTCTGCC | TGTCACCTTC | ACTTCCGCAC | TCATCACTGC | ACTGAGTGTG | GGGGACTTGG | 480 |
| GCTCAGGATG | TCCAGAGACG | TGGTTCCGCC | CCCTCNCTTA | ATGACACCGN | CCANNCAACC | 540 |
| GTCGGCTCCC | GCCGANTGNG | TTCGTCGTNC | CTGGGTCAGG | GTCTGCTGGC | CNCTACTTGC | 600 |
| AANCTTCGTC | NGGCCCCATGG | AATTCAACCNC | ACCGGAACTN | GTANGATCCA | CTNNNTCTAT | 660 |
| AACCGGNCGC | CACCGCENNNT | GGAACTCCAC | TCTTNTINCC | TTTACTTGAG | GGTTAAGGTC | 720 |
| ACCCCTNNCG | TTACCTTGGT | CCAAACCNNT | CCNTGTGTCG | ANATNGTNAA | TCNGGNCCNA | 780 |
| TNCCANCCNC | ATANGAAGCC | NG | | | | 802 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | | | | |
|------------|--------------|------------|------------|------------|-------------|-----|
| CNAAGCTTCC | AGGTNACGGG | CCGCNAANCC | TGACCCNAGG | TANCANAANG | CAGNCNGCGG | 60 |
| GAGCCCACCG | TCACGNGGNG | GNGTCTTTAT | NGGAGGGGGC | GGAGCCACAT | CNCTGGACNT | 120 |
| CNTGACCCCA | ACTCCCCNCC | NCNCANTGCA | GTGATGAGTG | CAGAACTGAA | GGTNACGTGG | 180 |
| CAGGAACCAA | GANCAAANNC | TGCTCCNNTC | CAAGTCGGCN | NAGGGGGCGG | GGCTGGCCAC | 240 |
| GCNCATCCNT | CNAGTGTGCTGN | AAAGCCCCNN | CCTGTCTACT | TGTTTGGAGA | ACNGCENNNGA | 300 |
| CATGCCAGN | GTTANATAAAC | NGGCNGAGAG | TNANTTTGCC | TCTCCCTTCC | GGCTGCGCAN | 360 |
| CGNGTNTGCT | TAGNGGACAT | AACCTGACTA | CTTAACTGAA | CCCNNGAATC | TNCCNCCCCCT | 420 |
| CCACTAAGCT | CAGAACAAAA | AACTTCGACA | CCACTCANTT | GTCACCTGNC | TGCTCAAGTA | 480 |
| AAGTGTACCC | CATNCCCAAT | GTNTGCTNGA | NGCTCTGNCC | TGCNTTANGT | TCGGTCCTGG | 540 |
| GAAGACCTAT | CAATTNAAGC | TATGTTTCTG | ACTGCCTCTT | GCTCCCTGNA | ACAANCNACC | 600 |
| CNNCNNTCCA | AGGGGGGGNC | GGCCCCCAAT | CCCCCCAACC | NTNAATTNAN | TTTANCCCCN | 660 |
| CCCCCNGGCC | CGGCCTTTA | CNANCNTCNN | NNACNGGGNA | AAACCNNNGC | TTTNCCCAAC | 720 |
| NNAATCCNCC | T | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | AAAAACCCC | CTCCATTNAA | TGNAAACTTC | CGAAATTGTC | 60 |
| CAACCCCCTC | NTCAAATNN | CCNTTCCGG | GNGGGGTTC | CAAACCCAAN | TTANNTTTGG | 120 |
| ANNTTAAATT | AAATNTNNT | TGGNGNNNA | ANCCNAATGT | NANGAAAGTT | NAACCCANTA | 180 |
| TNANCTTNAA | TNCCTGGAAA | CCNGTNGNTT | CACAAAATNT | TTAACCCCTTA | ANTCCCTCCG | 240 |
| AAATNGTTNA | NGGAAAACCC | AANTTCTCNT | AAGGTTGTTT | GAAGGNTNAA | TNAAAANCCC | 300 |
| NNCCAATTGT | TTTNGCCAC | GCCTGAATTA | ATTGGNTTCC | GNTGTTTCC | NTTAAAANAA | 360 |
| GGNNANCCCC | GGTTANTNAA | TCCCCCNNC | CCCAATTATA | CCGANTTTT | TTNGAATTGG | 420 |
| GANCCNCGG | GAATTAACGG | GGNNNNNTCCC | TNTTGGGGGG | CNNGNNCCCC | CCCCNTCGGG | 480 |
| GGTTNGGGNC | AGGNCNNAAT | TGTTTAAGGG | TCCGAAAAAT | CCCTCCNAGA | AAAAAAANCTC | 540 |
| CCAGGNTGAG | NNTNGGGTTT | NCCCCCCCCC | CANGCCCCCT | CTCGNANAGT | TGGGGTTTGG | 600 |
| GGGGCCTGGG | ATTTNTTTC | CCCTNTTNCC | TCCCCCCCCC | CCNGGGANAG | AGGTTNGNGT | 660 |
| TTTGNTCNNC | GGCCCCNCCN | AAGANCTTN | CCGANTTNAN | TTAAATCCNT | GCCTNGGCAGA | 720 |
| AGTCCNTIGN | AGGGNTAAAN | GGCCCCCTNN | CGGG | | | 754 |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ATCANCCCAT | GACCCNAAC | NNGGGACCN | TCANCCGGNC | NNNCNACCNC | CGGCCNATCA | 60 |
| NNGTNAGNNC | ACTNCNNTTN | NATCACNCCC | CNCCNACTAC | GCCCNCNANC | CNACGCNCTA | 120 |
| NNCANATNCC | ACTGANNGCG | CGANGTNGAN | NGAGAAANCT | NATACCANAG | NCACCCANACN | 180 |
| CCAGCTGTCC | NANAANGCCT | NNNATACNGG | NNNATCCAAT | NTGNANCTC | CNAAGTATTN | 240 |
| NNCNNCANAT | GATTTCTTN | ANCCGATTAC | CCNTNCCCCC | TANCCCCTCC | CCCCAACNA | 300 |
| CGAAGGCNCT | GGNCCNAAGG | NNGCGNCNCC | CCGCTAGNTC | CCCNCAAGT | CNCNCNCCTA | 360 |
| AACTCANCCN | NATTACNCGC | TTCNTGAGTA | TCACTCCCCG | AATCTCACCC | TACTCAACTC | 420 |
| AAAANATCN | GATACAAAAT | AATNCAAGCC | TGNTTATNAC | ACTNTGACTG | GGTCTCTATT | 480 |
| TTAGNGGTCC | NTNAANCNTC | CTAATACTTC | CAGTCTNCCT | TCNCCAATTT | CCNAANGGCT | 540 |
| CTTTCNGACA | GCATNTTTG | GTTCCCNNTT | GGGTTCTTAN | NGAATTGCC | TTCNTNGAAC | 600 |
| GGGCTCNTCT | TTTCCTTCGG | TTANCCTGGN | TCNNCCGGC | CAGTTATTAT | TTCCCNNTTT | 660 |
| AAATTCTNCC | CNTTANTTT | TGGCNTTCNA | AACCCCCGGC | CTTGAAAACG | GCCCCCTGGT | 720 |
| AAAAGGTTGT | TTTGANAAAA | TTTTGTTTT | GTTCC | | | 755 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|------------|-------------|------------|-------------|-------------|------------|-----|
| TTTTTTTTT | TTTTTANGTG | TNGTCGTGCA | GGTAGAGGCT | TACTACAANT | GTGAANACGT | 60 |
| ACGCTNGGAN | TAANGCGACC | CGANTTCTAG | GANNCCNCCCT | AAAATCANAC | TGTGAAGATN | 120 |
| ATCCTGNNNA | CGGAANGGTC | ACCGGNNGAT | NNTGCTAGGG | TGNCCNCTCC | CANNNCNTTN | 180 |
| CATAACTCNG | NGGCCCTGCC | CACCACCTTC | GGCGGCCNG | NGNCCGGGC | CGGGTCATTN | 240 |
| GNNTTAACCN | CACTNNGCNA | NCGGTTTCCN | NCCCCNNCNG | ACCCNGGCGA | TCCCCGGTNC | 300 |
| TCTGTCTTCC | CCTGNAGNCN | ANAAANTGGG | CCNCGGNCCC | CTTTACCCCT | NNACAAGCCA | 360 |
| CNGCCNTCTA | NCCNCNGCCC | CCCCTCCANT | NNGGGGACT | GCCNANNGCT | CCGTTNCTNG | 420 |
| NNACCCNNN | GGGTNCCTCG | GTTGTCGANT | CNACCGNANG | CCANGGATT | CNAAGGAAGG | 480 |
| TGCGTTNTTG | GCCCCTACCC | TTCGCTNCGG | NNCACCCCTTC | CCGACNANGA | NCCGCTCCCG | 540 |
| CNCNCNGNNG | CCTCNCCCTCG | CAACACCCGC | NCTCNTCNGT | NCGGNNNNCCC | CCCCACCCGC | 600 |
| NCCCTNCNC | NGNCGNANCN | CTCCNCCNCC | GTCTCANNCA | CCACCCCGCC | CCGCCAGGCC | 660 |
| NTCANCCACN | GGNNGACNNG | NAGCNCNNTC | GCNCCGCGCN | CGGNCCNCC | CGCCNCNGAA | 720 |
| CTNCNTCNGG | CCANTNNCGC | TCAANCCNA | CNAAACGCCG | CTGCGGGCC | CGNAGCGNCC | 780 |
| NCCTCCNCGA | GTCCTCCGN | CTTCNNACCC | ANGNNTTCCN | CGAGGACACN | NNACCCCGCC | 840 |
| NNCANGCGG | | | | | | 849 |

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| GCGCAAACTA | TACTTCGCTC | GNACTCGTGC | GCCTCGCTNC | TCTTTTCCTC | CGCAACCATG | 60 |
| TCTGACNANC | CCGATTNGGC | NGATATCNAN | AAGNTCGANC | AGTCCAAACT | GANTAACACA | 120 |
| CACACNCNAN | AGANAAATCC | NCTGCCTTCC | ANAGTANACN | ATTGAACNNG | AGAACCCANGC | 180 |
| NGGCGAATCG | TAATNAGGCG | TGCGCCGCCA | ATNTGTCNCC | GTTTATTNTN | CCAGCNTCNC | 240 |
| CTNCCNACCC | TACNTCTTCN | NAGCTGTCTN | ACCCCTNGTN | CGNACCCCCC | NAGGTGGGA | 300 |
| TCGGGTTTNN | NNTGACCGNG | CNNCCCTCC | CCCCNTCCAT | NACGANCNC | CCGCACCACC | 360 |
| NANNGCNGC | NCCCCGNCT | CTTCGCCNCC | CTGTCCCTTN | CCCCTGTNGC | CTGGCNCNGN | 420 |
| ACCGCATTGA | CCCTCGCCNN | CTNCNNGAAA | NCGNANACGT | CCGGGTTGNN | ANNANCCTG | 480 |
| TGGGNNNGCG | TCTGCNCCCG | GTTCTTCCN | NCNNCTTCCA | CCATCTTCNT | TACNGGTCT | 540 |
| CCNCGCCNTC | TCNNNCACNC | CCTGGGACGC | TNTCCTNTGC | CCCCCTTNAC | TCCCCCCCCTT | 600 |
| CGNCGTGNCC | CGNCCCCACC | NTCATTNCA | NACGNTCTTC | ACAANNNCCT | GGNTNNCTCC | 660 |
| CNANCNGNCN | GTCANCCNAG | GGAAAGGGNGG | GGNNCCNNTG | NTTGACGTTG | NGGGNGANGTC | 720 |
| CGAANANTCC | TCNCCNTCAN | CNCTACCCCT | CGGGCGNNCT | CTCNGTTNCC | AACTTANCAA | 780 |
| NTCTCCCCCG | NGNGCNCNTC | TCAGGCTCNC | CCNCCCNCT | CTCTGCANTG | TNCTCTGCTC | 840 |
| TNACCNNTAC | GANTNTTCGN | CNCCCTCTTT | CC | | | 872 |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | |
|---|-----|
| GCATGCAAGC TTGAGTATTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA | 60 |
| NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA | 120 |
| TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTCNGAN CANATTCCCA TNNATTNCGN | 180 |
| CGCATTNCNC GCNCANTATN TAATNGGGAA NTCNNNTNNN NCACCNNCAT CTATCNTNCC | 240 |
| GCNCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN | 300 |
| AANANCCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT | 360 |
| AACCTGCGTC AGANNCATCA AACNTGGAA ACCCGCNCC ANGTNNAAGT NGNNNCANAN | 420 |
| GATCCCCTGAGGNTTNAACC ATCCCTTCNC AGCGCCCCCT TTNGTGCCCTT ANAGNGNAGC | 480 |
| GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGGCA CAATGTCGNC | 540 |
| GAACCCCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCCNANC | 600 |
| CCCNCCCTAC CCNNCTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GCCNGNCTC | 660 |
| CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCGAGGN NTCGNAAGGA | 720 |
| ACCGGNCTN GGNCGAANNG ANCNNTCNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA | 780 |
| NCCNACNGNT AGNTCCCCCCC CNGGGTNCGG AANGG | 815 |

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 775 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | |
|--|-----|
| CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG | 60 |
| AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCAGC TCATCCAGCA GAGAATGGAA | 120 |
| AGTCAAATTT CCTGAATTGC TATGTGTCTG GGTTTCATCC ATCCGACATT GAANTTGACT | 180 |
| TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTC AGACTTGTCT TTCAGCAAGG | 240 |
| ACTGGTCTTT CTATCTCNG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG | 300 |
| CCTGCCGTGT GAACCATGTG ACTTTGTAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA | 360 |
| TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCGGCATTG GATTGGATGA ATTCCAAATT | 420 |
| CTGCTTGCTT GCNTTTAAT ANTGATATGC NTATACACCC TACCCTTAT GNCCCCAAAT | 480 |
| TGTAGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCNTTCG | 540 |
| AATTGCCGT CNCCNGTTN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC | 600 |
| TCTTACGGAA GGGCCTGGGC CNCTTNCAA GTTGGGGGA ACCNAAAATT TCNCTNTGC | 660 |
| CCNCCCNCCA CNNTCTTGNG NNCNCANTTT GGAACCCCTC CNATTCCCCT TGGCCTCNNA | 720 |
| NCCTTNCTA ANAAAACCTN AAACGTNGC NAAANNTTN ACTTCCCCCCC TTACC | 775 |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|--|-----|
| ANATTANTAC AGTGTAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC | 60 |
| CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC | 120 |
| GAAGGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCAGAG GGGTGAGTAG | 180 |
| CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA | 240 |
| NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA | 300 |
| NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC | 360 |
| TTCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCTG GGANCAGCTA | 420 |
| ACNNAGCACT CACCTGCCCC CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT | 480 |
| CCCTGTTGGA ATTNCGGGA NACCAAGGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAANN | 540 |
| GATGGAATTG TNCCCTTCGG GCCNNNTCCCC TCTTCCTTITA CACGCCCT NNTACTCNC | 600 |
| TCCCTCTNTT NTCCGTGNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TCGGANNCTN | 660 |
| GANATTCCAC TNNCGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT | 720 |
| GGGNNCCTCG NTCATCCTCT CTTTTCNCT ACCNCCNNTT CTTTGCCTCT CCTTNGATCA | 780 |
| TCCAACCNTC GNTGGCCNTN CCCCCCNNTN TCCTTTNCC | 820 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|--|-----|
| TCTGGGTGAT GGCCTTTCC TCCTCAGGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT | 60 |
| TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTTCAGCCCT GCCAACCTG ATTCTGATGA | 120 |
| CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGCGC | 180 |
| CTGCTGAGCA CTTCCGCCCC TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGTC | 240 |
| TCCGCCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC | 300 |
| TTCTTCCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCTGTGC ANGCNCCTTG | 360 |
| GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTTCTGANN TCTTCANTTA ACTNTGANTT | 420 |
| TATNACCNA TGGNCTGTNC TGTCCNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC | 480 |
| NCTCCCTTCC ANTCNNNA ACCNGCTTNC CNTCNCTC CCNTANCCCG CCNGGGAAANC | 540 |
| CTCCTTGTCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC | 600 |
| CTGNTNNNNCC CNCTCNCTN TNCCCTGTC CCNNNNCGCN NNGCANNTTC NCNGTCCNN | 660 |
| TNNCTCTTCN NGNTCGNA NGNTCNCNTN TNNNNNNGNCN NGNTNNNTNCN TCCCTCTCNC | 720 |
| CNNNTGNANG TNNTTNNNNC NCNGNNCCCC NNNNNNNNNN NGGNNTNNN TCTNCNCNGC | 780 |
| CCNNCCCCC NGNATTAAGG CCTCCNNCTC CCGGCCNC | 818 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| AGGAAGGGCG | GAGGGATATT | GTANGGGATT | GAGGGATAGG | AGNATAANGG | GGGAGGTGTG | 60 |
| TCCAACATG | ANGGTGNNGT | TCTCTTTGA | ANGAGGGTTG | NGTTTTANN | CCNGGTGGGT | 120 |
| GATTNAACCC | CATTGTATGG | AGNAAAGGN | TTTNAGGGAT | TTTCGGCTC | TTATCAGTAT | 180 |
| NTANATTCCCT | GTNAATCGGA | AAATNATNTT | TCNNCNGGAA | AATNTTGCTC | CCATCCGNA | 240 |
| ATTNCTCCCG | GGTAGTGCAT | NTTNGGGGGN | CNGCCANGTT | TCCCAGGCTG | CTANAATCGT | 300 |
| ACTAAAGNTT | NAAGTGGGAN | TNCAAATGAA | AACCTNNAC | AGAGNATCCN | TACCGACTG | 360 |
| TNNNTTNCCT | TCGCCCTNTG | ACTCTGCNNG | AGCCAATAC | CCNNNGNAT | GTCNCCNGN | 420 |
| NNNGCGNCNC | TGAAANNNNC | TCGNNGCTNN | GANCATCANG | GGGTTTCGCA | TCAAAGCNN | 480 |
| CGTTTCNCAT | NAAGGCACCT | TNGCCTCATC | CAACCNCNTNG | CCCTCNCCCA | TTTNGCCGTC | 540 |
| NGGTTCNCCCT | ACGCTNNTNG | CNCCTNNNTN | GANATTTNC | CCGCCTNGGG | NAANCCTCCT | 600 |
| GNAATGGGTA | GGGNCTTNTC | TTTNAACCNN | GNGGTNTACT | AATCNNTNC | ACGCNTNCTT | 660 |
| TCTCNACCCCC | CCCCCTTTT | CAATCCCANC | GGCNAATGGG | GTCTCCCN | CGANGGGGG | 720 |
| NNNCCCANNC | C | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGNCNC | TTCTATGANT | ANTNTTAGAT | 60 |
| CGCTCANACC | TCACANCCTC | CCNACNANGC | CTATAANGAA | NANNAATAGA | NCTGTNCNN | 120 |
| ATNTNTACNC | TCATANNCTT | CNNNACCCAC | TCCCTTTAA | CCCNTACTGT | GCCTATNGCN | 180 |
| TNNCTANTCT | NTGCCGCCTN | CNANCCACCN | GTGGGCCNAC | CNCNNGNATT | CTCNATCTCC | 240 |
| TCNCCATNTN | GCCTANANTA | NGTNCATACC | CTATACCTAC | NCCAATGCTA | NNNCTAANCN | 300 |
| TCCATNANTT | ANNNTAACTA | CCACTGACNT | NGACTTTCNC | ATNANCTCCT | AATTGAAATC | 360 |
| TACTCTGACT | CCCACNGCCT | ANNNATTAGC | ANCNTCCCCC | NACNATNTCT | CAACCAAATC | 420 |
| NTCAACAACC | TATCTANCTG | TTCNCCAACC | NTTNCCCTCCG | ATCCCCNNAC | AACCCCCCTC | 480 |
| CCAAATACCC | NCCACCTGAC | NCCTAACCN | CACCATCCCC | GCAAGCCNAN | GGNCATTAN | 540 |
| CCACTGGAAT | CACNATNGGA | AAAAAAAAC | CCNAACTCTC | TANCNNAT | CTCCCTAANA | 600 |
| AATNCTCTN | NAATTTACTN | NCANTNCCAT | CAANCCACN | TGAAACNNAA | CCCCCTGTTTT | 660 |
| TANATCCCTT | CTTCGAAAA | CCNACCCCTT | ANNNCCCAAC | CTTNGGGCC | CCCCCNCTNC | 720 |
| CCNAATGAAG | GNCNCCCAAT | CNANGAAACG | NCCNTGAAAA | ANCNAGGCNA | ANANNNTCCG | 780 |
| CANATCCTAT | CCCTTANTTN | GGGGNCCCTT | NCCCNNGGCC | CC | | 822 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| CGGCCGCCTG | CTCTGGCACA | TGCCTCCTGA | ATGGCATCAA | AAAGTGATGGA | CTGCCCATTG | 60 |
| CTAGAGAAGA | CCTCTCTCC | TACTGTCATT | ATGGAGCCCT | GCAGACTGAG | GGCTCCCCCTT | 120 |
| GTCTGCAGGA | TTTGATGCT | GAAGTCGTGG | AGTGTGGCTT | GGAGCTCCTC | ATCTACATNA | 180 |
| GCTGGAAGCC | CTGGAGGCC | TCTCTGCCA | GCCTCCCCCT | TCTCTCACG | CTCTCCANGG | 240 |
| ACACCAGGGG | CTCCAGGCAG | CCCATTATTC | CCAGNANGAC | ATGGTGTTTC | TCCACGCGGA | 300 |
| CCCATGGGGC | CTGNAAGGCC | AGGGTCTCCT | TTGACACCAT | CTCTCCCGTC | CTGCCTGGCA | 360 |
| GGCCGTGGGA | TCCACTANTT | CTANAACGGN | CGCCACCNCG | GTGGGAGCTC | CAGCTTTTGT | 420 |
| TCCCNTTAAT | GAAGGTTAAT | TGNCNCCTTG | GCGTAATCAT | NGGTCANAAC | TNTTCCCTGT | 480 |
| GTGAAATTGT | TTNTCCCTC | NCNATTCCNC | NCNACATACN | AACCCGGAAN | CATAAAAGTGT | 540 |
| TAAAGCCTGG | GGGTNGCCTN | NNGAATNAAC | TNAACTCAAT | TAATTGCGTT | GGCTCATGGC | 600 |
| CCGCTTCCN | TTCNGGAAAA | CTGTCNTCCC | CTGCNTNNNT | GAATCGGCCA | CCCCCCNGGG | 660 |
| AAAAGCGGTT | TGCNTTTTNG | GGGGNTCCTT | CCNCTTCCCC | CCTCNCTAAN | CCCTNCGCCT | 720 |
| CGGTGTTNC | NGGTNGGGGG | GAANGGGNAT | NNNCTCCNC | NAAGGGGGNG | AGNNNGNTAT | 780 |
| CCCCAAA | | | | | | 787 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | |
|-------------|------------|------------|-------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTGGC | GATGCTACTG | TTTAATTGCA | GGAGGGGGGG | GTGTGTGTAC | 60 |
| CATGTACCAAG | GGCTATTAGA | AGCAAGAAGG | AAGGAGGGAG | GGCAGAGCGC | CCTGCTGAGC | 120 |
| AACAAAGGAC | TCCTGCAGCC | TTCTCTGTCT | GTCTCTTGGC | GCAGGCACAT | GGGGAGGCCT | 180 |
| CCCGCAGGGT | GGGGGCCACC | AGTCCAGGGG | TGGGAGCACT | ACANGGGGTG | GGAGTGGGTG | 240 |
| GTGGCTGGTN | CNAATGGCCT | GNCACANATC | CCTACGATTTC | TTGACACCTG | GATTCACCA | 300 |
| GGGGACCTTC | TGTTCTCCCA | NGGNAACTTC | NTNNATCTCN | AAAGAACACA | ACTGTTTCTT | 360 |
| CNGCANTTCT | GGCTGTTCAT | GGAAAGCACA | GGTGTCCNAT | TTNGGCTGGG | ACTTGGTACA | 420 |
| TATGGTTCCG | GCCCACCTCT | CCCNTCNAAN | AAGTAATTCA | CCCCCCCCCN | CCNTCTNTTG | 480 |
| CCTGGGCCCT | TAANTACCCA | CACCGGAAC | CANTTANTTA | TTCATCTTNG | GNTGGGCTTG | 540 |
| NTNATCNCCN | CCTGAANGCG | CCAAGTTGAA | AGGCCACGCC | GTNCCCNCTC | CCCATAGNAN | 600 |
| NTTTTNNCN | CANCTAATGC | CCCCCNNGGC | AACNATCCAA | TCCCCCCCCN | TGGGGGGCCCC | 660 |
| AGCCCANGGC | CCCCGNCTCG | GGNNNCCNGN | CNCGNANTCC | CCAGGNTCTC | CCANTCNGNC | 720 |
| CCNNNGCNCC | CCCGCACCGA | GAACANAAGG | NTNGAGCCNC | CGCANNNNNN | NGGTNNNCNAC | 780 |
| CTCGCCCCCCC | CCNNCGNNG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| TTTNCCNAG | GGCAGGTTTA | TTGACAACCT | CNCGGGACAC | AANCAGGCTG | GGGACAGGAC | 120 |
| GGCAACAGGC | TCCGGCGCG | GCGGCGGCGG | CCCTACCTGC | GGTACCAAAT | NTGCAGCCTC | 180 |
| CGCTCCCGCT | TGATNTTCT | CTGCAGCTGC | AGGATGCCNT | AAAACAGGGC | CTCGGCCNTN | 240 |
| GGTGGGCACC | CTGGGATTNN | AATTCCACG | GGCACAATGC | GGTCGCANCC | CCTCACCACC | 300 |
| NATTAGGAAT | AGTGGTNTTA | CCCNCCNCCG | TTGGCNCACT | CCCCNTGGAA | ACCACTTNTC | 360 |
| GCGGCTCCGG | CATCTGGTCT | TAAACCTTGC | AAACNCTGGG | GCCCTCTTTT | TGGTTANTNT | 420 |
| NCCNGCCACA | ATCATNACTC | AGACTGGCNC | GGGCTGGCCC | AAAAAAANCN | CCCCAAAACC | 480 |
| GGNCCATGTC | TTNNCGGGGT | TGCTGCNATN | TNCATCACCT | CCCGGGCNCA | NCAGGNCAAC | 540 |
| CCAAAAGTTC | TTGNGGCCN | AAAAAAANCT | CCGGGGGGNC | CCAGTTCAA | CAAAGTCATC | 600 |
| CCCCTTGGCC | CCCAAATCCT | CCCCCGNTT | NCTGGGTTTG | GGAACCCACG | CCTCTNNCTT | 660 |
| TGGNNGGCAA | GNTGGNTCCC | CCTTCGGGCC | CCCGGTGGGC | CCNCTCTAA | NGAAAACNCC | 720 |
| NTCCTNNNCA | CCATCCCCC | NNGNNACGNC | TANCAANGNA | TCCCTTTTT | TANAAACGGG | 780 |
| CCCCCCNCG | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| GACAGAACAT | GTTGGATGGT | GGAGCACCTT | TCTATACGAC | TTACAGGACA | GCAGATGGGG | 60 |
| AATTATGGC | TGTTGGAGCA | ATANAACCCC | AGTTCTACGA | GCTGCTGATC | AAAGGACTTG | 120 |
| GAECTAAAGTC | TGATGAACTT | CCCAATCAGA | TGAGCATGGA | TGATTGGCCA | GAAATGAANA | 180 |
| AGAAAGTTGC | AGATGTATTT | GCAAAGAAGA | CGAAGGCAGA | GTGGTGTCAA | ATCTTGACG | 240 |
| GCACAGATGC | CTGTGTGACT | CCGGTTCTGA | CTTTTGAGGA | GGTTGTTCAT | CATGATCACA | 300 |
| ACAANGAACG | GGGCTCGTT | ATCACCANTG | AGGAGCAGGA | CGTGAGCCCC | CGCCCTGCAC | 360 |
| CTCTGCTGTT | AAACACCCCA | GCCATCCCTT | CTTCAAAAG | GGATCCACTA | CTTCTAGAGC | 420 |
| GGNCGCCACC | GCGGTGGAGC | TCCAGCTTTT | GTTCCCTTTA | GTGAGGGTTA | ATTGCGCGCT | 480 |
| TGGCGTAATC | ATGGTCATAN | CTGTTTCTG | TGTGAAATTG | TTATCCGCTC | ACAATTCCAC | 540 |
| ACAACATACG | ANCCGGAAGC | ATNAAATTTT | AAAGCCTGGN | GGTNGCCTAA | TGANTGAACT | 600 |
| NACTCACATT | AATTGGCTTT | GCGCTCACTG | CCCGCTTTCC | AGTCCGGAAA | ACCTGTCCCT | 660 |
| GCCAGCTGCC | NTTAATGAAT | CNGGCCACCC | CCCGGGGAAA | AGGCNGTTG | CTTNTTGGGG | 720 |
| CGCNCTTCCC | GCTTTCTCGC | TTCCTGAANT | CCTTCCCCCC | GGTCTTTCGG | CTTGCAGGCNA | 780 |
| ACGGTATCNA | CCT | | | | | 793 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCGCGACCG | GCATGTACGA | GCAACTCAAG | GGCGAGTGG | ACCGTAAAG | CCCCAATCTT | 60 |
| ANCAAGTGCG | GGGAANAGCT | GGGTGACTC | AAGCTAGTTC | TTCTGGAGCT | CAACTTCTT | 120 |
| CCAACCACAG | GGACCAAGCT | GACCAAACAG | CAGCTAATT | TGGCCCGTGA | CATACTGGAG | 180 |
| ATCGGGGCC | AATGGAGCAT | CCTACGCAAN | GACATCCCCT | CCTTCGAGCG | CTACATGGCC | 240 |
| CAGCTCAAAT | GCTACTACTT | TGATTACAAN | GAGCAGCTCC | CCGAGTCAGC | CTATATGCAC | 300 |
| CAGCTCTTGG | GCCTCAACCT | CCTCTTCCTG | CTGTCCCAGA | ACCGGGTGGC | TGANTNCCAC | 360 |
| ACGGANTTGG | ANCGGCTGCC | TGCCCAANGA | CATACANACC | AATGTCTACA | TCNACCACCA | 420 |
| GTGTCTTGG | GCAATACTGA | TGGANGGCAG | CTACCNAAA | GTNTTCTGG | CCNAGGGTAA | 480 |
| CATCCCCCGC | CGAGAGCTAC | ACCTTCTTC | TTGACATCCT | GCTCGACACT | ATCAGGGATG | 540 |
| AAAATCGCNG | GGTTGCTCCA | GAAAGGCTNC | AANAANATCC | TTTTCNCTGA | AGGCCCGGG | 600 |
| ATNCNCTAGT | NCTAGAATCG | GCCCCGCATC | GGGGTGGANC | CTCCAACCTT | TCGTTNCCCT | 660 |
| TTACTGAGGG | TTNATTGCCG | CCCTGGCGT | TATCATGGTC | ACNCCNGTN | CCTGTGTTGA | 720 |
| AATTNTTAAC | CCCCCACAAT | TCCACGCCNA | CATTNG | | | 756 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| GGGGATCTCT | ANATCNACCT | GNATGCATGG | TTGTCGGTGT | GGTCGCTGTC | GATGAANATG | 60 |
| AACAGGATCT | TGCCCTTGAA | GCTCTCGGCT | GCTGTNTTA | AGTTGCTCAG | TCTGCCGTCA | 120 |
| TAGTCAGACA | CNCTCTTGGG | CAAAAAACAN | CAGGATNTGA | GTCTTGATTT | CACCTCCAAT | 180 |
| AATCTTCNGG | GCTGTCTGCT | CGGTGAACTC | GATGACNANG | GGCAGCTGGT | TGTGTNTGAT | 240 |
| AAANTCCANC | ANGTTCTCCT | TGGTGACCTC | CCCTTCAAG | TTGTTCCGGC | CTTCATCAA | 300 |
| CTTCTNNAAAN | ANGANNANCC | CANCTTTGTC | GAGCTGGNAT | TTGGANAACA | CGTCACTGTT | 360 |
| GGAAACTGAT | CCCAATGGT | ATGTCATCCA | TCGCCTCTGC | TGCCTGCAAA | AAACTTGCTT | 420 |
| GGCNCAAATC | CGACTCCCCN | TCCTTGAAAG | AAGCCNATCA | CACCCCCCTC | CCTGGACTCC | 480 |
| NNCAANGACT | CTNCCGCTNC | CCCNCTCCNNG | CAGGGTTGGT | GGCANNCCGG | GCCCCNTGCGC | 540 |
| TTCTTCAGCC | AGITTCACNAT | NTTCATCAGC | CCCTCTGCCA | GCTGTTNTAT | TCCTGGGGG | 600 |
| GGAAANCCGTC | TCTCCCTTCC | TGAANNAACT | TTGACCGTNG | GAATAGCCGC | GCNTCNCCNT | 660 |
| ACNTNCTGGG | CCGGGTTCAA | ANTCCCTCCN | TTGNCNNTCN | CCTCGGGCCA | TTCTGGATTT | 720 |
| NCCNAACTTT | TTCCCTCCCC | CNCCCCNCGG | NGTTTGGNTT | TTTCATNGGG | CCCCAACTCT | 780 |
| GCTNTTGGCC | ANTCCCCTGG | GGGCNTNTAN | CNCCCCCTNT | GGTCCCNNTNG | GGCC | 834 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|-----|
| CGGNCGCTTT | CCNGCCGCGC | CCCCTTCCA | TGACNAAGGC | TCCCTTCANG | TTAAATACNN | 60 |
| CCTAGNAAAC | ATTAATGGGT | TGCTCTACTA | ATACATCATA | CNAACCAGTA | AGCCTGCCA | 120 |
| NAACGCCAAC | TCAGGCCATT | CCTACCAAAG | GAAGAAAGGC | TGGTCTCTCC | ACCCCTGTA | 180 |
| GGAAAGGCCT | GCCTTGTAAAG | ACACCACAAT | NCGGCTGAAT | CTNAAGTCTT | GTGTTTTACT | 240 |
| AATGGAAAAAA | AAAAATAAAC | AANAGGTTT | GTTCTCATGG | CTGCCACCG | CAGCCTGGCA | 300 |
| CTAAAACANC | CCAGCGCTCA | CTTCTGCTTG | GANAAATATT | CTTGCTCTT | TTGGACATCA | 360 |
| GGCTTGATGG | TATCACTGCC | ACNTTTCAC | CCAGCTGGC | NCCCTTCCCC | CATNTTTGTC | 420 |
| ANTGANCTGG | AAGGCCTGAA | NCTTAGTCTC | CAAAGTCTC | NGCCCACAAG | ACCGGCCACC | 480 |
| AGGGGANGTC | NTTNCAGTG | GATCTGCCA | ANANTACCCN | TATCATCNNT | GAATAAAAAG | 540 |
| GCCCCTGAAC | GANATGCTTC | CANCANCCTT | TAAGACCCAT | AATCCTNGAA | CCATGGTGCC | 600 |
| CTTCCGGTCT | GATCCNAAG | GAATGTTCT | GGGTCCANT | CCCTCCTTTG | TTNCTTACGT | 660 |
| TGTNTTGGAC | CCNTGCTNGN | ATNACCAAN | TGANATCCCC | NGAAGCACCC | TNCCCCCTGGC | 720 |
| ATTIGANTTT | CNTAAATTCT | CTGCCCTACN | NCTGAAAGCA | CNATTCCCTN | GGCNCCNAAN | 780 |
| GGNGAACTCA | AGAAGGTCTN | NGAAAAACCA | CNCN | | | 814 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| GCATGCTGCT | CTTCCTCAAA | GTTGTTCTTG | TTGCCATAAC | AACCACCATA | GGTAAAGCGG | 60 |
| GCGCAGTGT | CGCTGAAGGG | GTTGTAGTAC | CAGCGCGGG | TGCTCTCCTT | GCAGAGTCCT | 120 |
| GTGTCTGGCA | GGTCCACGCA | ATGCCCTTG | TCACTGGGG | AATGGATGCG | CTGGAGCTCG | 180 |
| TCNAANCCAC | TCGTGTATT | TTCACANGCA | GCCTCCTCCG | AAGCNTCCGG | GCAGTTGGGG | 240 |
| GTGTCGTAC | ACTCCACTAA | ACTGTCGATN | CANCAGCCCA | TTGCTGCAGC | GGAACTGGGT | 300 |
| GGGCTGACAG | GTGCCAGAAC | ACACTGGATN | GGCCTTTCCA | TGGAAGGGCC | TGGGGGAAAT | 360 |
| CNCCTNANCC | CAAACAGCCT | CTCAAAGGCC | ACCTTGACACA | CCCCGACAGG | CTAGAAATGC | 420 |
| ACTCTTCTTC | CCAAAGGTAG | TTGTTCTTGT | TGCCCAAGCA | NCCTCCANCA | AACCAAAANC | 480 |
| TTGAAAATC | TGCTCCGTGG | GGGTCATNNN | TACCANGTT | GGGGAAAANAA | ACCCGGCNGN | 540 |
| GANCCNCCTT | GTTTGAATGC | NAAGGNAATA | ATCCTCCTGT | CTTGCTTGGG | TGGAANAGCA | 600 |
| CAATTGAACT | GTAAACNTG | GGCCGNGTTC | CNCTNGGGTG | GTCTGAAACT | AATCACCGTC | 660 |
| ACTGGAAAAAA | GGTANGTGCC | TTCCTTGAAT | TCCCAAANTT | CCCCTNGNTT | TGGGTNNNTT | 720 |
| CTCCTCTNCC | CTAAAATCG | TNTTCCCCCC | CCNTANGGCG | | | 760 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTAAAAAA | CCCCCTCCAT | TGAATGAAAA | 60 |
| CTTCCNAAAT | TGTCCAACCC | CCTCNCCAA | ATNNCCATT | CGGGGGGGGG | GTTCCAAACC | 120 |

| | |
|---|-----|
| CAAATTAATT TTGGANTTTA AATTAAATNT TNATNGGGG AANAANCAA ATGTNAAGAA | 180 |
| AATTAAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAATTTAAC | 240 |
| CTTAATCCC TCCGAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT | 300 |
| NGATTTAAC CCCCTTNANT TNTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGT | 360 |
| TCCTNTTAAN CNTNGGTAAC TCCCCNTAAT GAANNNCCT AANCCAATTA AACCGAATT | 420 |
| TTTTGAATT GGAAATTCCN NGGGATTNA CCGGGGTTT TCCCNTTGG GGGCATNCC | 480 |
| CCCNCTTCG GGGTTGGGN NTAGGTTGAA TTTTNNANG NCCCCAAAAA NCCCCAANA | 540 |
| AAAAAACTCC CAAGNNTAA TTNGAATNTC CCCCTTCCC GGCCTTTGG GAAAGGNGGG | 600 |
| TTTNTGGGG CCNNGGANTT CNTTCCCCN TTNCCNCCCC CCCCCCNNGT AAANGTTAT | 660 |
| NGNNNTTGGT TTTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAT CCCGGGNCG | 720 |
| GCCG | 724 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | |
|--|-----|
| TTTTTTTTTT TTTTTCTTTG CTCACATTAA ATTTCATTT TGATTTTTT TAATGCTGCA | 60 |
| CAACACAATA TTTATTTCAT TTGTTCTTT TATTCATTT TATTGTTTG CTGCTGCTGT | 120 |
| TTTATTATT TTTACTGAAA GTGAGAGGGAA ACTTTGTGG CCTTTTTCTC TTTTCTGTA | 180 |
| GGCCGCCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT | 240 |
| CGCAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTGTAA TCATGCCCTA TGGTGGGTGA | 300 |
| TTAACTGCTT GTACAATTAC NTTTCACTTT TAATTAATTG TGCTNAANGC TTTAATTANA | 360 |
| CTTGGGGGTT CCCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG | 420 |
| TCCCGGCNT CNTGAAACA CACNGCNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAA | 480 |
| TGAAGGGTTA CCATNTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN | 540 |
| CCCTCAANCN AAATTCTNNG CCCCAGTCNC GCNTNNGTCC CNCCCCGGCT CGGGGAANTN | 600 |
| CACCCCCNGA ANNCNTNNNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC | 660 |
| CNNAGACTNT CCTCNANCN CNCAATTTC TTTTNTAC GAACNCGNNC CNNAAAATGN | 720 |
| NNNNNCNCCTC CNTGTCCTN NAATCNCCAN C | 751 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | |
|---|-----|
| GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCCTCAT | 60 |
| AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGG GTAGGGAGGG | 120 |
| CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA | 180 |
| TGGTCTGGAA CGGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAACT | 240 |
| TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGT | 300 |

| | |
|---|-----|
| CGGTATAAN CGCGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCTCCCGC AGGAAGGCNA | 360 |
| ATAAAAGGTG CGCCCCCGCA CCGTTCANCT CGCACTTCTC NAANACCATG ANGTTGGGCT | 420 |
| CNAACCCACC ACCANNCCCG ACTTCCTTGA NGGAATTCCC AAATCTCTC GNTCTTGGC | 480 |
| TTCTNCTGAT GCCCTANCTG GTTGCCNGN ATGCCAANCA NCCCCAANCC CGGGGTCCT | 540 |
| AAANCACCCN CCTCCTCNNT TCATCTGGT TTTNTCCCC GGACCNNTGGT TCCTCTCAAG | 600 |
| GGANCCATA TCTCNACCAN TACTCACCN NCCCCCCNT GNNACCCANC CTTCTANNGN | 660 |
| TTCCCNCCCG NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC | 720 |
| TNCCCTATCT GNACCCCN CN TTTGTCTCAN TNT | 753 |

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | |
|---|-----|
| ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG | 60 |
| AGTGAACCCA TCCTTGATT ATATACATAT ATGTTCTCAG TATTTTGGGA GCCTTCCAC | 120 |
| TTCTTAAAC CTTGTTCATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTTAAAAAGT | 180 |
| TATAGCTTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACA CTTAGTTGAG | 240 |
| TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTTCAGAG GTATTTCAT | 300 |
| TTTACTTT TGATTAATTG TGTTTATAT ATTAGGGTAG T | 341 |

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | |
|--|-----|
| ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTGAT | 60 |
| GTTCACAAACA TTCTAAATAA ATAATTTCA GTGGCTTCAT A | 101 |

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACATCTTTGT | TACAGTCTAA | GATGTGTTCT | AAATCACCA | TTCCTCCTG | GTCCTCACCC | 60 |
| TCCAGGGTGG | TCTCACACTG | TAATTAGAGC | TATTGAGGAG | TCTTACAGC | AAATTAAGAT | 120 |
| TCAGATGCCT | TGCTAAGTCT | AGAGTCTAG | AGTTATGTTT | CAGAAAGTCT | AAGAAACCCA | 180 |
| CCTCTTGAGA | GGTCAGTAA | GAGGACTTAA | TATTCATAT | CTACAAAATG | ACCACAGGAT | 240 |
| TGGATACAGA | ACGAGAGTTA | TCCTGGATAA | CTCAGAGCTG | AGTACCTGCC | CGGGGGCCGC | 300 |
| TCGAA | | | | | | 305 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| ACATAAAATAT | CAGAGAAAAG | TAGTCTTTGA | AAATATTACG | TCCAGGAGTT | CTTTGTTTCT | 60 |
| GATTATTTGG | TGTGTGTTTT | GGTTTGTGTC | CAAAGTATTG | GCAGCTTCAG | TTTCATTTT | 120 |
| CTCTCCATCC | TCGGGCATTC | TTCCCCAAATT | TATATACCAAG | TCTTCGTCCA | TCCACACGCT | 180 |
| CCAGAATTTC | TCTTTTGTAG | TAATATCTCA | TAGCTCGGCT | GAGCTTTCA | TAGGTCTATGC | 240 |
| TGCTGTTGTT | CTTCTTTTTA | CCCCATAGCT | GAGCCACTGC | CTCTGATTTC | AAGAACCTGA | 300 |
| AGACGCCCTC | AGATCGGTCT | TCCCATTAA | TTAACCTGG | GTTCTTGTCT | GGGTTCAAGA | 360 |
| GGATGTCGCG | GATGAATTCC | CATAAGTGAG | TCCCTCTCGG | TTTGTGCTTT | TTGGTGTGGC | 420 |
| ACTTGGCAGG | GGGGTCTTGC | TCCTTTTCA | TATCAGGTGA | CTCTGCAACA | GGAAGGTGAC | 480 |
| TGGTGGTTGT | CATGGAGATC | TGAGCCCGGC | AGAAAGTTTT | GCTGTCCAAC | AAATCTACTG | 540 |
| TGCTACCATA | GTTGGTGTCA | TATAAATAGT | TCTNGTCTTT | CCAGGTGTTTC | ATGATGGAAG | 600 |
| GCTCAGTTTG | TTCAGTCTTG | ACAATGACAT | TGTGTGTTGA | CTGGAACAGG | TCACTACTGC | 660 |
| ACTGGCCGTT | CCACTTCAGA | TGCTGCAAGT | TGCTGTAGAG | GAGNTGCCCC | GCCGTCCCTG | 720 |
| CCGGCCGGGT | GAACCTCTGC | AAACTCATGC | TGCAAAGGTG | CTCGCCGTTG | ATGTCGAACT | 780 |
| CNTGGAAAGG | GATACAATTG | GCATCCAGCT | GGTTGGTGTG | CAGGAGGTGA | TGGAGCCACT | 840 |
| CCACACCTG | GT | | | | | 852 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|--|-----|
| ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG | 60 |
| AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT | 120 |
| GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG | 180 |
| TGAACGTGTC GGTGGGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT | 234 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|--|-----|
| ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA | 60 |
| ATTTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA | 120 |
| AAGAAGATAAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA | 240 |
| AAAGCTTTCA AAANAAAANAA TTATTGCACT CTANNTAATT CAAACAGTGT TAAATGGTAT | 300 |
| CAGGATAAAAN AACTGAAGGG CANAAAGAAAT TAATTTTCAC TTICATGTAAC NCACCCANAT | 360 |
| TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAAGTANTC AAGGTCTTTC | 420 |
| TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT | 540 |
| GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT | 590 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|---|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC | 60 |
| TGAACAGAAT TTTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC | 120 |

| | |
|--|-----|
| GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AACAGAAAAG GGGACAAAGG CTAATCCAA | 240 |
| AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGA CAACTGACCA TGCCCCAGG CTCCTGTGTG | 360 |
| CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC | 420 |
| CCACACTCCT TGAACACACA TCCCCAGTT ATATTCCTGG ACATGGCTGA ACCTCCTATT | 480 |
| CCTACTCCG AGATGCCCTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC | 540 |
| ACGGCATGGG AAGCCTTTCT GACTTGCCCTG ATTACTCCAG CATCTTGAA CAATCCCTGA | 600 |
| TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACCAGCTATG GGACCTGGGG CAAGTNATCT | 720 |
| TCACTTCTAT GGGCNTCATT TTGTTCTACC TGAAAATGG GGGATAATAA TAGT | 774 |

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|---|-----|
| CANAAAATTGAA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT | 60 |
| TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCCCTT AATTACAGCT CAACGCAACT | 120 |
| TGGT | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|---|-----|
| GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT | 60 |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT | 120 |
| TTAGGGCACC CATATCCAA GCANTGT | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC 60
 ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT 107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGAA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG 60
 CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG 120
 GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCA CACTTGGCCA 180
 CCTCCCTTT GGGACCAGCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA 60
 GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAA AGTTAGAAAT GTATAAAACA 120
 CCATCAGACA GGTTTTAAA AAACAAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA 180
 AAAACTTCTT GTATCAATT CTTTGTTC AATGACTGA CTTAANTATT TTTAAATATT 240
 TCANAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCC 300
 ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC 360
 ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT 420

| | |
|--|-----|
| CAATTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT | 480 |
| ATCACTCTTG T | 491 |

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| ACATAATTAA GCAGGGCTAA TTACCATAG ATGCTATTAA TTAANAGGTN TATGATCTGA | 60 |
| GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC | 120 |
| ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT | 180 |
| CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTTGAAATCT | 240 |
| GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC | 300 |
| AGCTTTGANT TTCTTTGTC TGATANGAGG AAAGGCTGAA TTACCTTGTG GCCTCTCCCT | 360 |
| AATGATTGGC AGGTGNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCCNCG | 420 |
| TANCTTGANT CTGTGTATTG CAGGANCAGG CGGATGGAAT GGGCCAGCCC NC GGATGTTTC | 480 |
| CANT | 484 |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|--|-----|
| ACTAAACCTC GTGTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG | 60 |
| CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAACAC AAATCCTTGG CACTGGCTAG | 120 |
| TCTATGTCCT CTCAAGTGCC TTTTTGTTTG T | 151 |

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | |
|---|----|
| ACCTGGCTTG TCTCCGGGTG GTTCCCGCG CCCCCCACGG TCCCCAGAAC GGACACTTC | 60 |
| GCCTCCAGT GGATACTCGA GCCAAAGTGG T | 91 |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | |
|--|-----|
| GGCGGAATGTG CGTIGGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT | 60 |
| TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC | 120 |
| AAGGGACAAC TGT | 133 |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|---|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC | 60 |
| GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGGT | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC | 60 |
| TGATTACATA CATTATCCT TTAAAAAAGA TGTAAATCTT AATTTTATG CCATCTATTA | 120 |
| ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT | 180 |
| TTGACTTCTA AGTTGGGT | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|-----|
| ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT | 60 |
| CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTC | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG | 240 |
| CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTTGAAGAGT | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60 |
| GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC | 120 |
| TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | | | | | | | | |
|------------|-----|------------|------------|-----|----------|------------|------------|-----|
| ACCCCAC | TTT | TCCTCCTGTG | AGCAGTCTGG | AC | TTCTCACT | GCTACATGAT | GAGGGTGAGT | 60 |
| GGTTGTTG | C | CTTCAACAGT | ATCCTCC | CTT | CCGGATCT | GCTGAGCCGG | ACAGCAGTGC | 120 |
| TGGACTGCAC | AG | CCCCGGGG | CTCCACATTG | CT | GT | | | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

| | | | |
|------------|------------|------------|----|
| CGCTCGAGCC | CTATAGTGAG | TCGTATTAGA | 30 |
|------------|------------|------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | | | | | | | |
|------------|---------|-------|------------|------------|-----------|------------|----|
| ACAAGTCATT | TCAGCAC | CCT | TTGCTCTTCA | AAACTGACCA | TCTTTATAT | TTAATGCTTC | 60 |
| CTGTATGAAT | AAA | ATGGT | ATGTCAAGT | | | | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | |
|---|----------|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT | 60 97 |
|---|----------|

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|---|--|
| ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCT TTTGATGGCA GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGTTTGG GCTNTCCCAA ACCGCACACC CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGCGA TGCAANGGTG CCAACAGGAG GGCGGGAGG AGCATGT | 60 120 180 240 300 360 377 |
|---|--|

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | |
|--|----|
| ACGCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG | 60 |
|--|----|

| | |
|---|-----|
| AGAACCCGTG TGCCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG | 120 |
| AGGAACAAAC TGCACCCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT | 180 |
| TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT | 240 |
| TTATATATTT TTTAATAAGA TGCACTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC | 300 |
| TGTTT | 305 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|--|-----|
| ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTGTCC CAGCACTTTA GGAATGCTGA | 60 |
| GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC | 120 |
| CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC | 180 |
| TGTGCTGTCC TGGAGATTCA CTTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTAGAGG | 240 |
| CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG | 300 |
| CCTCTCCCAAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACACTCAG ATGCCCATAC | 360 |
| CATAGTTCT GTGCTAGTGG ACCGT | 385 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|--|----|
| ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA | 60 |
| GTTTTTTAA TGG | 73 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGGCTC | TCACCCCTCCT | CTCCTGCAGC | 60 |
| TCCAGCTTTG | TGCTCTGCCT | CTGAGGAGAC | CATGGCCAG | CATCTGAGTA | CCCTGCTGCT | 120 |
| CCTGCTGGCC | ACCCTAGCTG | TGGCCCTGGC | CTGGAGCCCC | AAGGAGGAGG | ATAGGATAAT | 180 |
| CCCGGTGGC | ATCTATAACG | CAGACCTCAA | TGATGAGTGG | GTACAGCGTG | CCCTTCACCT | 240 |
| CGCCATCAGC | GAGTATAACA | AGGCCACCAA | AGATGACTAC | TACAGACGTC | CGCTGCGGGT | 300 |
| ACTAAGAGCC | AGGCAACAGA | CCGTTGGGGG | GGTGAATTAC | TTCTTCGACG | TAGAGGTGGG | 360 |
| CCGAACCATA | TGTACCAAGT | CCCAGCCAA | CTTGGACACC | TGTGCCTTCC | ATGAACAGCC | 420 |
| AGAACTGCAG | AAGAAACAGT | TGTGCTCTT | CGAGATCTAC | GAAGTTCCCT | GGGGAGAACAA | 480 |
| GAANGTCCCT | GGGTGAAATC | CAGGTGTCAA | GAAATCCTAN | GGATCTGTTG | CCAGGC | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| ATGACCCCTA | ACAGGGGCC | TCTCAGCCCT | CCTAATGACC | TCCGGCCTAG | CCATGTGATT | 60 |
| TCACTTCCAC | TCCATAACGC | TCCTCATACT | AGGCCTACTA | ACCAACACAC | TAACCATATA | 120 |
| CCAATGATGG | CGCGATGTAA | CACGAGAAAG | CACATACCAA | GGCCACCACA | CACCACTGTC | 180 |
| CCAAAAAGGC | CTTCGATACG | GGATAATCCT | ATTATTATTAC | TCAGAAGTTT | TTTTCTTCGC | 240 |
| AGGGATTTTT | CTGAGCCTTT | TACCACTCCA | GCCTAGCCCC | TACCCCCCAA | CTAGGAGGGC | 300 |
| ACTGGCCCCC | AACAGGCATC | ACCCCGCTAA | ATCCCCTAGA | AGTCCCACTC | CTAAACACAT | 360 |
| CCGTATTACT | CGCATCAGGA | GTATCAATCA | CCTGAGCTCA | CCATAGTCTA | ATAGAAAACA | 420 |
| ACCGAAACCA | AATTATTCAA | AGCACTGCTT | ATTACAATT | TACTGGGTCT | CTATTTT | 477 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|-----|
| AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCACACACA | 60 |
| AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCTTA | 120 |
| ATAATGGTAA GATTGGTTA | 180 |
| TGTGATTTA GTGGTATTT TGGCACCCCTT ATATATGTTT | 240 |
| TCCAAACTTT CAGCAGTGAT | 300 |
| ATTATTTCCA TAACCTAAAA AGTGAGTTTG AAAAAGAAAA | 360 |
| TCTCCAGCAA GCATCTCATT | 420 |
| TAAATAAAGG TTGTCATCT TAAAAAATAC AGCAATATGT | 480 |
| GACTTTTAA AAAAGCTGTC | 533 |
| AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT | |
| TAAAAACATC GAGTACCTCA | |
| AGTCAGTTG CTTGAAAAA TATCAAATAT AACTCTTACA | |
| GAAATGTACA TAAAAGAATG | |
| CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCATTGTTG | |
| TATTTTAAA AAGTACATGG | |
| TAAAAAAA AATTACACAC AGTATATAAG GCTGTAAAAT | |
| GAAGAATTCT GCC | |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | |
|--|-----|
| TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA | 60 |
| ANACTGCTTC AGGGCGTGTAA | 120 |
| AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC | 180 |
| TAAAAGAGGG ACAAGGCTAA | 240 |
| AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG | 300 |
| TTGGCTGGAG GAGCTGTGGA | 360 |
| AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT | 420 |
| CCTCATTGTT ATTACANAGT | 480 |
| GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC | 511 |
| AATAATGATA GAATAGTACA | |
| CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC | |
| CAACTAGATC CTCAGAAANAC | |
| GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC | |
| TTGTGCCCTT GTCTGTTATG | |
| ATTCTCTCC ATTGCAGCNA NAAACCGTT CTTCTAAGCA AACNCAGGTG | |
| ATGATGGCNA | |
| AAATACACCC CCTCTTGAAG NACCNGGAGG A | |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | |
|---|-----|
| CAGTGCCAGC ACTGGTGCCA GTACCAAGT CAATAACAGT | 60 |
| GCCAGTGCCA GTGCCAGCAC | 120 |
| CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT | 180 |
| CTCACATTG GGCTCTTCGC | 240 |
| TGGCCTTGGT GGAGCTGGTG CCAGCACCAG TGGCAGCTCT | |
| GGTGCCTGTG GTTTCTCCTA | |
| CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTC | |
| TCTTCAAGCC AGGGTGCATC | |

| | | |
|---|----------------------------------|-----|
| CTCAGAAACC TACTAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT | GAAGTTGACA | 300 |
| CTCTGCATTA AATCTATTG CCATTCTGA AAAAAAAA | AAAAAAAGGG CGGCCGCTCG | 360 |
| ANTCTAGAGG GCCCGTTAA ACCCGCTGAT CAGCCTCGAC | TGTGCCTCT ANTTGCCAGC | 420 |
| CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT | TCCTTGACCC TGGAAAGTGC CACTCCCACT | 480 |
| GTCCTTCCCT AANTAAAAT | | 499 |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | |
|--|------------|-----|
| TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTG GGATTCA | GCGAAGAGAT | 60 |
| TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA | GTCTCTAACT | 120 |
| TCCAGGCCCA CGGCTCAAGT GAATTGAAAT ACTGCATTG CAGTGTAGAG | TAACACATAA | 180 |
| CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT | CTAATCAAGA | 240 |
| AAAGAATTAC AGACTCTGAT TCTACAGTG TGATTGAAATT CTAAAATGG | TAATCATTAG | 300 |
| GGCTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA | TACTGCCTTC | 360 |
| CAGTTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTG AATGGGTTCT | 420 | |
| ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA | CACTCTTGAT | 480 |
| TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA | GTCCCGT | 537 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | | |
|--|------------|-----|
| CAAANACAAT TGTTCAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA | CAAACACCTC | 60 |
| TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTG | GCCATCATCA | 120 |
| CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA | TAACAGACGG | 180 |
| TGGACAAGG AGGCCATCTT TTCTCATCG GTTATTGTCC CTAGAACGT | CTTCTGAGGA | 240 |
| TCTAGTTGGG CTTTCTTCTT GGGTTGGC CATTTCANTT CTCATGTGT | TACTATTCTA | 300 |
| TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAC | TCTGTAATAA | 360 |
| CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTNT | TCCAGAGCTC | 420 |
| CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACAA | TCCCTGN | 467 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | |
|---|-----|
| AAGCTGACAG CATTGGGCC GAGATGTCTC GCTCCGTGGC CTTAGCTGTG CTCGCGCTAC | 60 |
| TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAAGTT TACTCACGTC | 120 |
| ATCCAGCAGA GAATGGAAAG TCAAATTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT | 180 |
| CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG | 240 |
| ACTTGCTTT CAGCAAGGAC TGGTCTTCT ATCTCTTGTGTA CTACACTGAA TTCACCCCCA | 300 |
| CTGAAAAAGA TGAGTATGCC TGCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG | 360 |
| TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT | 400 |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|---|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT | 60 |
| CCAGCTGCC CGGCGGGGGG TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC | 120 |
| CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA | 180 |
| GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA | 240 |
| AAAAAAAAAA | 248 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTAACA | 60 |
| TCACCCAGAC CCCGCCCTGC CCGTCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT | 180 |
| GATTAAAAAA AAAAAAAA A | 201 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | |
|--|-----|
| TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG | 60 |
| TTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCTT ATTCTTTATT | 120 |
| CCTCTTCTT CTGAAGATTAA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG | 180 |
| TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT | 240 |
| ATGCAAGTTA GAAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT | 300 |
| CTGTCCTTG GCTAGAAAAA ATTATAAACAA GGACTTTGTT AGTTGGGAA GCCAAATTGA | 360 |
| TAATATTCTA TGTTCTAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TCCAATTAA | 420 |
| TTCCCAAGGAA TATGGGGTTC ATTTATGAAAT ANTACCCGGG ANAGAAGTT TGANTNAAAC | 480 |
| CNGTTTGTT TAATACGTTA ATATGCTCTN AATNAACAAG GCNTGACTTA TTTCAAA | 540 |
| AAAAAAA AA | 552 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | |
|--|-----|
| ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCCTCT TATTTTCAGA | 60 |
| GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT | 120 |
| CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT | 180 |
| GCAATTCACTG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA | 240 |
| AGGTTAAACT TTCCCAACCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC | 300 |

| | | |
|---|----------------------------|-----|
| TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT | GGGGGTTGAT AGGAANTNTC | 360 |
| TCTGGCTT CTCATAAAA TCTCTATCCA TCTCATGTTT | AATTTGGTAC GCNTAAAAAT | 420 |
| GCTGAAAAAA TTAAATGTT CTGGTTTCNC | TTTAAAAAAA AAAAAAAA AAAAAA | 476 |

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | | | | |
|-----------------------|-----------------------|-------------|-------------|-----|
| TTTTTTTTTG TATGCCNTCN | CTGTGGNGTT ATTGTTGCTG | CCACCCCTGGA | GGAGCCCGAGT | 60 |
| TTCTTCTGTA | TCTTCTTTT | CTGGGGGATC | TTCCTGGCTC | 120 |
| CTCATCCCCA | TCTTGCACCT | TTGCTAGGGT | TGGAGGCGCT | 180 |
| ACTCAGTCAG | CGGGAAATAAG | TCCTAGGGT | GGGGGGTGTG | 232 |
| | | | GCAAGCCGGC | CT |

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| AGGCAGGGAGC | AGAAGCTAAA | GCCAAAGCCC | AAGAAGAGTG | GCAGTGCCAG | CACTGGTGCC | 60 |
| AGTACCAAGTA | CCAATAACAT | GCCAGTGCCA | GTGCCAGCAC | CAGTGGTGGC | TTCAGTGCTG | 120 |
| GTGCCAGCCT | GACCGCCACT | CTCACATTTG | GGCTCTTCGC | TGGCCTGGT | GGAGCTGGTG | 180 |
| CCAGCACCAG | TGGCAGCTCT | GGTGCCTGTG | TTTCTCCTA | CAAGTGAGAT | TTTAGATATT | 240 |
| GTTAACCTG | CCAGTCTTC | TCTTCAAGCC | AGGGTGCATC | CTCAGAAACC | TACTCAACAC | 300 |
| AGCACTCTNG | GCAGCCACTA | TCAATCAATT | GAAGTTGACA | CTCTGCATTA | AATCTATTG | 360 |
| CCATTTCAAA | AAAAAAA | AAA | | | | 383 |

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | |
|--|-----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA | 60 |
| GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC | 120 |
| CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA | 180 |
| ACGCTTCAAG GTGCTCATGAA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG | 240 |
| ATGCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG | 300 |
| AGCCCTGATG CCTTTTTGCC AGCCATACTC TTGGCNTCC AGTCTCTCGT GGCGATTGAT | 360 |
| TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT | 420 |
| TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA | 480 |
| AAAAAAAAAA AAAAA | 494 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | |
|--|-----|
| GCTGGTAGCC TATGGCGTGG CCACGGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA | 60 |
| AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG | 120 |
| GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG | 180 |
| GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCCTCTCCC AGTATGCCAA CTGGCTGGTG | 240 |
| GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCAAACATCC TGCTGGTCAC TTGCTCATTG | 300 |
| CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC | 360 |
| AGCGTTNCCG CCTCATCCGG | 380 |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| GAGTTAGCTC | CTCCACAAACC | TTGATGAGGT | CGTCTGCAGT | GGCCTCTCGC | TTCATACCGC | 60 |
| TNCCATCGTC | ATACTGTAGG | TTTGCCACCA | CCTCCTGCAT | CTTGGGGCGG | CTAATATCCA | 120 |
| GGAAACTCTC | AATCAAGTCA | CCGTCNATNA | AAACCTGTGGC | TGGTTCTGTC | TTCCGCTCGG | 180 |
| TGTGAAAGGA | TCTCCAGAAG | GAGTGCTCGA | TCTTCCCCAC | ACTTTTGATG | ACTTTATTGA | 240 |
| GTGCAATTCTG | CATGTCCAGC | AGGAGGTTGT | ACCAGCTCTC | TGACAGTGAG | GTCACCAGCC | 300 |
| CTATCATGCC | NTTGAACGTG | CCGAAGAACAA | CCGAGCCTTG | TGTGGGGGT | GNAGTCTCAC | 360 |
| CCAGATTCTG | CATTACCAGA | NAGCCGTGGC | AAAAGANATT | GACAACCTCGC | CCAGGNNGAA | 420 |
| AAAGAACACC | TCCTGGAAGT | GCTNGCCGCT | CCTCGTCCNT | TGGTGGNNNGC | GCNTNCCTTT | 480 |
| T | | | | | | 481 |

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| AACATCTTCC | TGTATAATGC | TGTGTAATAT | CGATCCGATN | TTGTCTGCTG | AGAATTCAATT | 60 |
| ACTTGGAAAA | GCAACTTNA | GCCTGGACAC | TGGTATTAAA | ATTCACACATA | TGCAACACTT | 120 |
| TAAACAGTGT | GTCAATCTGC | TCCCTTACTT | TGTCATCACC | AGTCTGGAA | TAAGGGTATG | 180 |
| CCCTATTACAC | ACCTGTTAAA | AGGGCGCTAA | GCATTTTGAA | TTCAACATCT | TTTTTTTTGA | 240 |
| CACAAGTCCG | AAAAAAAGCAA | AACTAAACAG | TTNTTAAATT | GTTAGCCAAT | TCACTTTCTT | 300 |
| CATGGGACAG | AGCCATTGAA | TTTAAAAAAGC | AAATTGCAAA | ATATTGAGCT | TTGGGAGCTG | 360 |
| ATATNTGAGC | GGAAGANTAG | CCTTTCTACT | TCACCAAGACA | CAAACCTTTT | CATATTGGGA | 420 |
| TGTTNACNA | AGTTATGTCT | CTTACAGATG | GGATGCTTTT | GTGGCAATT | TG | 472 |

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|-----|
| AGAAACCAGT | ATCTCTNA | ACAACCTCTC | ATACCTTGTG | GACCTAATTT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTT | TACTTTGTA | AAAGCTTATG | 120 |
| CCTCTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTC | TCTAGTTNGT | 240 |
| TTTATTGAC | ATGAAGGAAA | TTTCCAGATN | ACAAACACTNA | CAAACCTCTCC | CTTGACTAGG | 300 |
| GGGGACAAAG | AAAAGCNA | CTGAACATNA | GAAACAATTN | CCTGGTGAGA | AATTNCATAA | 360 |

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAACAGTTTTTT TTT

413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | |
|----------------------------------|-------------|-------------|-------------|-----|
| CGCAGCGGGT CCTCTCTATC TAGCTCCAGC | CTCTCGCCTG | CCCCACTCCC | CGCGTCCCGC | 60 |
| GTCCTAGCCN ACCATGGCCG | GGCCCCGCG | CGCCCCGCTG | CTCCCTGCTGG | 120 |
| CGTGGCCCTG GCCGTGAGCC | CCGCGGCCGG | CTCCAGTCCC | GGCAAGCCGC | 180 |
| GGGAGGCCCA TGGACCCCGC | GTGGAAGAAG | AAGGTGTGCG | CGGTGCAGT | 240 |
| TCGGCNANTA CAACAAACCC | GCAACNACTT | TTACCNAGCN | GACTTTGCCG | 300 |
| CCCAANCAAA TTGTTACTNG | GGGTAANTAA | TTCTTGGAAAG | GTGACCTGG | 360 |
| TTTACCAAGAA CCNAGCCAAT | TNGAACAAATT | NCCCTCCAT | GCCAAACNNG | 420 |
| GAANCANTCC TGNTCTTTTC | CAAATTTT | AACAGCCCT | TTTAAAAAGG | 448 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | | | | | |
|-----------------------|-------------|------------|------------|------------|-----|
| GAATTTGTG CACTGGCCAC | TGTGATGGAA | CCATTGGGCC | AGGATGCTTT | GAGTTTATCA | 60 |
| GTAGTGATTG TGCCAAAGTT | GGTGTGTAA | CATGAGTATG | AAAAATGTCA | AAAAATTAGC | 120 |
| AGAGGTCTAG GTCTGCATAT | CAGCAGACAG | TTTGTCCGTG | TATTTGTAG | CCTTGAAGTT | 180 |
| CTCAGTGACA AGTTNNTTCT | GATGCGAAGT | TCTNATTCCA | GTTGTTTAGT | CCTTTGCATC | 240 |
| TTTNATGTTN AGACTTGCT | CTNTNAAATT | GCTTTGTNT | TCTGCAGGTA | CTATCTGTGG | 300 |
| TTTAACAAAA TAGAANNACT | TCTCTGTTN | GAANATTGAA | ATATCTTACA | TCTNAAAATN | 360 |
| AATTCTCTCC CCATANNAAA | ACCCANGCCC | TTGGGANAAT | TTGAAAAANG | GNTCCTTCNN | 420 |
| AATTCNNANA ANTCAGNTN | TCATACAAACA | NAACNGGANC | CCC | | 463 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | | | | | |
|-----------------------|------------|------------|------------|------------|-----|
| AGGGATTGAA GGTCTNTNT | ACTGTCGGAC | TGTTCANCCA | CCAACTCTAC | AAGTTGCTGT | 60 |
| CTTCCACTCA CTGTCGTAA | GCNTNTAAC | CCAGACTGTA | TCTTCATAAA | TAGAACAAAT | 120 |
| TCTTCACCAG TCACATCTTC | TAGGACCTTT | TTGGATTCA | TTAGTATAAG | CTCTTCCACT | 180 |
| TCCTTTGTTA AGACTTCATC | TGGTAAAGTC | TTAAGTTTG | TAGAAAGGAA | TTTAATTGCT | 240 |
| CGTTCTCTAA CAATGTCCCT | TCCTTGAAGT | ATTGGCTGA | ACAACCCACC | TNAAGTCCCT | 300 |
| TTGTGCATCC ATTTTAAATA | TACTTAATAG | GGCATTGGTN | CACTAGGTTA | AATTCTGCAA | 360 |
| GAGTCATCTG TCTGCAAAAG | TTGCCTTAGT | ATATCTGCCA | | | 400 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | | | | | |
|------------------------|------------|------------|------------|-------------|-----|
| GAGCTCGGAT CCAATAATCT | TTGTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT | 60 |
| GGTCTACCCC ACATGGGAGC | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC | 120 |
| ATGCCTCTTT GACTACCGTG | TGCCAGTGC | GGTGATTCTC | ACACACCTCC | NNCCGCTCTT | 180 |
| TGTGGAAAAA CTGGCACTTG | NCTGAACTA | GCAAGACATC | ACTTACAAAT | TCACCCACGA | 240 |
| GACACTTGAA AGGTGTAAACA | AAGCGACTCT | TGCATTGCTT | TTTGTCCCTC | CGGCACCAAGT | 300 |
| TGTCAACTACT AACCCGCTGG | TTTGCTCTCA | TCACATTGTT | GATCTGTAGC | TCTGGATACA | 360 |
| TCTCCTGACA GTACTGAAGA | ACTTCTTCTT | TTGTTTCAA | AGCAACTCTT | GGTCCCTGTT | 420 |
| NGATCAGGTT CCCATTCCC | AGTCCGAATG | TTCACATGGC | ATATNTTACT | TCCCACAAAAA | 480 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|-----|
| ATACAGCCCC | NATCCCACCA | CGAAGATGCG | CTTGGTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGGTTGATGC | TGCACTCCTT | 120 |
| CCCACCGCAGG | CAGCAGCGGG | GCCGGTCAAT | GAACTCCACT | CGTGGCTTGG | GGTTGACGGT | 180 |
| TAANTGCAGG | AAGAGGCTGA | CCACCTCGCG | GTCCACCAGG | ATGCCCAGT | GTGCGGGACC | 240 |
| TGCAGCGAAA | CTCCTCGATG | GTCATGAGCG | GGAAGCGAAT | GANGCCCAGG | GCCTTGCCCCA | 300 |
| GAACCTTCCG | CCTGTTCTCT | GGCGTCAACCT | GCAGCTGCTG | CCGCTNACAC | TCGGCCCTCGG | 360 |
| ACCAGCGGAC | AAACGGCGTT | GAACAGCCGC | ACCTCACGGA | TGCCCANTGT | GTGCGCGCTCC | 420 |
| AGGAACGGCN | CCAGCGTGTG | CAGGTCAATG | TCGGTGAANC | CTCCGCGGGT | AATGGCG | 477 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|-----|
| GAACGGCTGG | ACCTTGCCCTC | GCATTGTGCT | GCTGGCAGGA | ATACCTTGGC | AAGCAGCTCC | 60 |
| AGTCCGAGCA | GCCCCAGACC | GCTGCCGCC | GAAGCTAAGC | CTGCCTCTGG | CCTTCCCCCTC | 120 |
| CGCCTCAATG | CAGAACCCANT | AGTGGGAGCA | CTGTGTTTAG | AGTTAAGAGT | GAACACTGTN | 180 |
| TGATTTTACT | TGGGAATTTC | CTCTGTTATA | TAGCTTTTCC | CAATGCTAAT | TTCCAAACAA | 240 |
| CAACACAAA | ATAACATGTT | TGCCTGTTNA | GTTGTATAAA | AGTANGTGAT | TCTGTATNTA | 300 |
| AAGAAAATAT | TACTGTTACA | TATACTGCTT | GCAANTTCTG | TATTTATTGG | TNCTCTGGAA | 360 |
| ATAAAATATAT | TATTAATA | | | | | 377 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CCCTTTGAGG | GGTTAGGGTC | CAGTTCCCAG | TGGAAGAAC | AGGCCAGGAG | AANTGCGTGC | 60 |
| CGAGGCTGANG | CAGATTTCCC | ACAGTGACCC | CAGAGCCCTG | GGCTATAGTC | TCTGACCCCT | 120 |
| CCAAGGAAAG | ACCACCTTCT | GGGGACATGG | GCTGGAGGGC | AGGACCTAGA | GGCACCAAGG | 180 |
| GAAGGCCCCA | TTCCGGGGCT | GTTCCCCGAG | GAGGAAGGGA | AGGGGCTCTG | TGTGCCCCCC | 240 |
| ACGAGGAANA | GGCCCTGANT | CCTGGGATCA | NACACCCCTT | CACGTGTATC | CCCACACAAA | 300 |

| | |
|---|-----|
| TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC | 360 |
| ACACCCACCC AGANCANCCA CCCGCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG | 420 |
| TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA | 480 |
| AAAAAAAANA AAAAAA | 495 |

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | |
|---|-----|
| GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC | 60 |
| CCTCTGGAAG CCTTGCAG AGCGGACTTT GTAATTGTT GAGAATAACT GCTGAATTT | 120 |
| TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACTC AATATGAAAA CTATTTNACT | 180 |
| TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTGT TCATACTGTA TTTATCAAGT | 240 |
| ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA | 300 |
| ATCGGCAAAA TGTGGAGTGT ATGTTCTTT CACAGTAATA TATGCCTTT GTAACTTCAC | 360 |
| TTGGTTATT TATTGTAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA | 420 |
| TTTANTTCAN TAATTCTTT CCTGTTTAC GTTAATTGG AAAAGAATGC AT | 472 |

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | |
|--|-----|
| CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT | 60 |
| GTGGTGAAT TTCAAAATTAT TATGTAACCTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT | 120 |
| TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT | 180 |
| ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNGCANAATG TTCTAGNTAT | 240 |
| AGCTGGATAC ATACNGGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCCAAAT | 300 |
| TGTGTTAGTC TCAATTCTTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT | 360 |
| GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAGTN ACATCTGCGT | 420 |
| TACAAAGTCT ATCTTCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT | 476 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | |
|---|-----|
| ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA | 60 |
| AAATAATGCT GCAAACCTAA TGTTCTTATG CAAATGGAA CGCTAATGAA ACACAGCTTA | 120 |
| CAATCGAAA TCAAAACTCA CAAGTGTCA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA | 180 |
| GATTGTGCTC CTTCGGATAT GATTGTTTCT CANATCTGG GCAATNTTCC TTAGTCAAAT | 240 |
| CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT | 300 |
| GTGATTATNA ATTAATCAC AAATTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT | 360 |
| NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG | 420 |
| TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC | 479 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | |
|--|-----|
| AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA | 60 |
| TGCTAGTTCC TGTCTATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA | 120 |
| TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA | 180 |
| AGTGATTTCAG TTCCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA | 240 |
| TGAAGCCACT CTGAACACGCC TGGTATCTA GATGAGAACA GAGAAAATAA GTCAGAAAAT | 300 |
| TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT | 360 |
| TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCTGGC CGTTTATGAA CTGACCACCC | 420 |
| TTTCCAATAA CCTTGACGCT CCTGAACCTTG CTCCCTCTGCG A | 461 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|----------------|------------|------------|------------|-----|
| GTGGCCGCGC | GCAGGGTGT | TTT CCTCGTACCG | CAGGGCCCCC | TCCCTCCCC | AGGCCTCCCT | 60 |
| CGGCGCTCT | GC | GGGGCCCGA | GGAGGAGCGG | CTGGCGGGTG | GGGGGAGTGT | 120 |
| CGGTGAGAAA | AGCCTTCTCT | AGCGATCTGA | GAGGCGTGCC | TTGGGGGTAC | C | 171 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60 |
| CGACTGCGAC | GACGGCGGCG | GCGACAGTCG | CAGGTGCAGC | GC | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGTCGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCCGGT | GAAGCGGGAG | GCCTCGGGGA | GCCCCTCGGG | AAGGGCGGCC | 240 |
| CGAGAGATAC | GCAGGTGCAG | GTGGCCGCC | | | | 269 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTGGAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTTGCA | 60 |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTCA | GTCAACTTCC | TTTGTCTGTGG | 120 |
| TTGATTGGTT | TGTCTTTATG | GGGGCGGGGT | GGGGTAGGGG | AAACGAAGCA | AATAACATGG | 180 |
| AGTGGGTGCA | CCCTCCCTGT | AGAACCTGGT | TACAAAGCTT | GGGGCAGTTC | ACCTGGTCTG | 240 |
| TGACCGTCAT | TTTCTTGACA | TCAATGTTAT | TAGAAGTCAG | GATATCTTTT | AGAGAGTCCA | 300 |
| CTGTTCTGGA | GGGAGATTAG | GGTTTCTTGC | CAAATCCAAC | AAAATCCACT | GAAAAAGTTG | 360 |
| GATGATCAGT | ACGAATAACCG | AGGCATATTC | TCATATCGGT | GGCCA | | 405 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | |
|--|-----|
| TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT | 60 |
| GGCACTTAAT CCATTTTAT TTCAAAATGT CTACAAATTT AATCCCATTA TACGGTATTT | 120 |
| TCAAAATCTA ATTATTCAA ATTAGCCAA TCCTTACCAA ATAATACCCA AAAATCAAAA | 180 |
| ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATAACGG CTGGTGTTTT | 240 |
| CAAAGTACAA TTATCTTAAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT | 300 |
| CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC | 360 |
| AAATCTTAGG GGAATATATAA CTTCACACGG GATCTTAACT TTTACTCACT TTGTTTATTT | 420 |
| TTTTAAACCA TTGTTGGGC CCAACACAAT GGAATCCCCC CTGGACTAGT | 470 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | |
|--|-----|
| TTTTTTTTT TTTTTTTG A CCCCCCTCTT ATAAAAAACCA AGTTACCATT TTATTTACT | 60 |
| TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC | 120 |
| TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTAA GCTTAAAATC TGCTAAAGT | 180 |
| GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGTAAAAC ATCCAATTTC | 240 |
| ATTTTTCTTG TCTTTAAAT TATCTAATCT TTCCATTTC TCCCTATTCC AAGTCATTT | 300 |
| GCTTCTCTAG CCTCATTTC TAGCTCTTAT CTACTATTAG TAAAGGGCTT TTTCTAAA | 360 |
| AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCAAT ATTTCTACCT | 420 |
| ACGTTAATAA AATAGCATT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTATGT | 480 |
| CCATTTAGT CACTAAACGA TATCAAAGTG CCAGAACGCA AAAGGTTGT GAACATTAT | 540 |
| TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G | 581 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| TTTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTT | 60 |
| CACTCTCTAG ATAGGGCATG AAGAAAAC TC ATCTTTCCAG CTTTAAAATA ACAATCAAAT | 120 |
| CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA | 180 |
| AGGAAATCTG TTCATTCTC TCATTCTAT AGTTATATCA AGTACTACCT TGCATATTGA | 240 |
| GAGGTTTTTC TTCTCTATT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT | 300 |
| TTCATGCAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATTA | 360 |
| CAAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAAC | 420 |
| AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTTAAATATC CAAAATAATT | 480 |
| AAAGGAACAT TTTTAGCCCTG GGTATAATTA GCTAATTACAC TTTACAAGCA TTTATTAGAA | 540 |
| TGAATTACACA TGTTATTATT CCTAGCCCAA CACAATGG | 578 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| TTTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATT AAAATTCTATA | 60 |
| GAAAAGTGCCTTACATTAA TAAAAGTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT | 120 |
| GTCTTGAACA CCAATATTAA TTTGAGGAAA ATACACCAAA ATACATTAAAG TAAATTATT | 180 |
| AAGATCATAG AGCTTGTAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA | 240 |
| AAATCCACTA TTAGCAAATA AATTACTATG GACTTCITGCTTAAATTG TGATGAATAT | 300 |
| GGGGTGTAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA | 360 |
| TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTTCTCAA TCTTTAAGG | 420 |
| GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTTCTA TGGAAGGATT | 480 |
| AGATATGTTT CCTTGCCCAA TATTAATTTA ATAATAATGT TTACTACTAG TGAAACCC | 538 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | | | | | | | |
|------------|---|------------|------------|-------------|------------|------------|-----|
| TTTTTTTTTT | T | TTTTAGTC | AAGTTTCTAT | TTTTATTATA | ATTAAGTCT | TGGTCATTTC | 60 |
| ATTTATTAGC | T | CTCGCAACTT | ACATATTAA | ATTAAGAAA | CGTTTAGAC | AACTGTACAA | 120 |
| TTTATAAATG | T | AAAGGTGCCA | TTATTGAGTA | ATATATTCCCT | CCAAGAGTGG | ATGTGTCCCT | 180 |
| TCTCCCACCA | A | ACTAATGAAC | AGCAACATTA | GTTTAATTTC | ATTAGTAGAT | ATACACTGCT | 240 |
| GCAAACGCTA | A | TTCTCTCTCT | CCATCCCCAT | GTGATATTGT | GTATATGTGT | GAGTTGGTAG | 300 |
| AATGCATCAC | A | ATCTACAAAT | CAACAGCAAG | ATGAAGCTAG | GCTGGGCTTT | CGGTGAAAAT | 360 |
| AGACTGTGTC | T | TGTCTGAATC | AAATGATCTG | ACCTATCCTC | GGTGGCAAGA | ACTCTTCGAA | 420 |
| CCGCTTCTC | T | AAAGGCGCTG | CCACATTGT | GGCTTTGC | ACTTGTTC | AAA | 473 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | | | | | | | |
|------------|---|-------------|------------|-------------|-------------|-------------|------|
| CGCCATGGCA | C | TGCAAGGGCA | TCTCGGTCA | GGAGCTGTCC | GGCCTGGCCC | CGGGCCCGTT | 60 |
| CTGTGCTATG | G | TGCTCTGGCTG | ACTTCGGGGC | CGCTGTGGTA | CGCGTGGACC | GGCCCGGCTC | 120 |
| CCGCTACGAC | G | GTGAGCCGCT | TGGGCGGGGG | CAAGCGCTCG | CTAGTGTCTGG | ACCTGAAGCA | 180 |
| GCCGCGGGGA | G | GCCGCCGTGC | TGCGGGGTCT | GTGCAAGCGG | TGGATGTGC | TGCTGGAGCC | 240 |
| CTTCCGCCGC | G | GGTGTATGG | AGAAACTCCA | GCTGGGCCA | GAGATTCTGC | AGCAGGGAAA | 300 |
| TCCAAGGCTT | A | ATTTATGCCA | GGCTGAGTGG | ATTGGCCAG | TCAGGAAGCT | TCTGCCGGTT | 360 |
| AGCTGGCCAC | A | GATATCAACT | ATTTGGCTTT | GTCAAGGTGTT | CTCTCAAAAA | TTGGCAGAAG | 420 |
| TGGTGAGAAT | C | CCGTATGCC | CGCTGAATCT | CCTGGCTGAC | TTTGCTGGTG | GTGGCCTTAT | 480 |
| GTGTGCACTG | G | GGCATTATAA | TGGCTTTTT | TGACCGACA | CGCACTGACA | AGGGTCAGGT | 540 |
| CATTGATGCA | A | AATATGGTGG | AAGGAACAGC | ATATTTAAGT | TCTTTCTGT | GGAAAACCTCA | 600 |
| GAAATCGAGT | T | CTGTTGGAAAG | CACCTCGAGG | ACAGAACATG | TTGGATGGTG | GAGCACCTT | 660 |
| CTATACGACT | T | TACAGGACAG | CAGATGGGG | ATTCACTGGCT | GTTGGAGCAA | TAGAACCCCA | 720 |
| GTTCTACGAG | C | CTGCTGATCA | AAGGACTTGG | ACTAAAGTCT | GATGAACCTTC | CCAATCAGAT | 780 |
| GAGCATGGAT | G | GATTGGCCAG | AAATGAAGAA | GAAGTTGCA | GATGTATTG | CAAAGAACAG | 840 |
| GAAGGCAGAG | A | TGGTGTCAA | TCTTGACGG | CACAGATGCC | TGTGTGACTC | CGGTTCTGAC | 900 |
| TTTGAGGAG | T | GTTGTTCATC | ATGATCACAA | CAAGGAACGG | GGCTCGTTA | TCACCAAGTGA | 960 |
| GGAGCAGGAC | G | GTGAGCCCCC | GCCCTGCACC | TCTGCTGTTA | AAACACCCAG | CCATCCCTTC | 1020 |
| TTTCAAAAGG | A | GATCCTTCA | TAGGAGAAC | CACTGAGGAG | ATACTTGAAAG | AATTGGATT | 1080 |
| CAGCCGCGAA | A | GAGATTTC | AGCTTAACTC | AGATAAAATC | ATTGAAAGTA | ATAAGGTAAA | 1140 |
| AGCTAGTCTC | T | TAACCTCCAG | GCCCACGGCT | CAAGTGAATT | TGAATACTGC | ATTTACAGTG | 1200 |
| TAGAGTAACA | C | CATAACATTG | TATGCATGGA | AACATGGAGG | AAACAGTATTA | CAGTGTCTA | 1260 |
| CCACTCTAAT | A | CAAGAAAAGA | ATTACAGACT | CTGATTCTAC | AGTGTATGATT | GAATTCTAAA | 1320 |
| AATGGTTATC | T | ATTAGGGCTT | TTGATTTATA | AAACTTTGGG | TACTTATACT | AAATTATGGT | 1380 |
| AGTTATTCTG | C | CCTTCCAGTT | TGCTTGATAT | ATTGTTGAT | ATTAAGATTC | TTGACTTATA | 1440 |
| TTTGAAATGG | T | GTTCTAGTGA | AAAAGGAATG | ATATATTCTT | GAAGACATCG | ATATACATTT | 1500 |
| ATTACACTC | G | TTGATTCTAC | AATGTAGAAA | ATGAGGAAAT | GCCACAAATT | GTATGGTGAT | 1560 |

AAAAAGTCACG TGAAACAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1620
 A 1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1 5 10 15
 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20 25 30
 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35 40 45
 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50 55 60
 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65 70 75 80
 Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85 90 95
 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
 100 105 110
 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
 115 120 125
 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
 130 135 140
 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
 145 150 155 160
 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
 165 170 175
 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
 180 185 190
 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
 195 200 205
 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

| | | |
|---|-----|-----|
| 290 | 295 | 300 |
| His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu | | |
| 305 | 310 | 315 |
| Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala | | |
| 325 | 330 | 335 |
| Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu | | |
| 340 | 345 | 350 |
| Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn | | |
| 355 | 360 | 365 |
| Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu | | |
| 370 | 375 | 380 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | |
|--|------|
| GGCACGAGGC TGC GCCAGGG CCTGAGCGGA GGC GGGGGCA GCCTGCCAG CGGGGGCCCC | 60 |
| GGGCCTGGCC ATGCCCTACT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC | 120 |
| CAGTGCACC TAGTGGCTCT CACCTGCTTC CTCCCTGGCG TGGGCTGCCG GCTGACCCCG | 180 |
| GGTTTGTACC ACCTGGGCG CACTGCTCTC TGCACTGACT TCATGGTTTT CACGGTGCAGG | 240 |
| CTGCTTCACA TCTTCACGGT CAACAAACAG CTGGGGCCCA AGATCGTCAT CGTGAGCAAG | 300 |
| ATGATGAAGG ACGTGTTCTT CTTCCCTTTC TTCTCTGGCG TGTGGCTGGT AGCTATGGC | 360 |
| GTGCCACGG AGGGGCTCCT GAGGCCACGG GACAGTGAAT TCCCAAGTAT CCTGCGCCGC | 420 |
| GTCTTCTACC GTCCCTACCT GCAGATCTTC GGGCAGATTG CCCAGGAGGA CATGGACGTG | 480 |
| GCCCTCATGG AGCACAGCAA CTGCTCGTCG GAGCCCGGCT TCTGGGCACA CCCTCCTGGG | 540 |
| GCCCAGGCGG GCACCTGCGT CTCCCAGTAT GCCAACCTGGC TGGTGGTGCT GTCCTCGTC | 600 |
| ATCTTCTGC TCGTGGCCAA CATCTGCTG GTCAACTTGC TCATTGCCAT TTTCAGTTAC | 660 |
| ACATTCGGCA AAGTACAGGG CAACAGCGAT CTCTACTGGA AGGCGCAGCG TTACCGCCTC | 720 |
| ATCCGGGAAT TCCACTCTCG GCCCCGCGCTG GCCCCGCCCT TTATCGTCAT CTCCCACTTG | 780 |
| CGCCCTCTGC TCAGGCAATT GTGCAGCGA CCCCCGGAGCC CCCAGCCGTC CTCCCCGGCC | 840 |
| CTCGAGCATT TCCGGGTTA CCTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGAA | 900 |
| TCGGTGCATA AGGAGAACTT TCTGCTGGCA CGCGCTAGGG ACAAGCGGGA GAGCGACTCC | 960 |
| GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAAACAGCT GGGACACATC | 1020 |
| CGCGAGTACG AACAGCGCCT GAAAGTGTG GAGCGGGAGG TCCAGCAGTG TAGCCGCGTC | 1080 |
| CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC TCTGCCCTTGC TGCCCCCAGG TGGGCCGCCA | 1140 |
| CCCCCTGACC TGCCTGGGTC CAAAGACTGA GCCCCTGCTGG CGGACTTCAA GGAGAAGGCC | 1200 |
| CCACAGGGGA TTTTGCTCCT AGAGTAAGGC TCATCTGGGC CTGGGCCCTC GCACCTGGTG | 1260 |
| GCCTTGTCCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTCAGGACC ACCTTTGGGA | 1320 |
| GTGTCATCCT TACAAACCCAC AGCATGCCCG GCTCCTCCCA GAACCAGTCC CAGCCTGGGA | 1380 |
| GGATCAAGGC CTGGATCCCG GGCCGTTATC CATCTGGAGG CTGCAGGGTC CTTGGGGTAA | 1440 |
| CAGGGACCAC AGACCCCTCA CCACTCACAG ATTCCCTACA CTGGGGAAAT AAAGCCATT | 1500 |
| CAGAGGAAAA AAAAAAAA AAAA | 1524 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| GGGAACCAGC | CTGCACGCC | TGGCTCCGGG | TGACAGCCGC | GCGCCTCGGC | CAGGATCTGA | 60 |
| GTGATGAGAC | GTGTCCCCAC | TGAGGTGCC | CACAGCAGCA | GGTGTGAGC | ATGGGCTGAG | 120 |
| AAGCTGGACC | GGCACCAAAG | GGCTGGCAGA | AATGGGCGCC | TGGCTGATTC | CTAGGCAGTT | 180 |
| GGCAGCAGCA | AGGAGGAGAG | GCCGCAGCTT | CTGGAGCAGA | GCCGAGACGA | AGCAGTTCTG | 240 |
| GAGTGCCTGA | ACGGCCCCCT | GAGCCCTACC | CGCCTGGCCC | ACTATGGTCC | AGAGGCTGTG | 300 |
| GGTGAGCCGC | CTGCTGCCGC | ACCGGAAAGC | CCAGCTTGTG | CTGGTCAACC | TGCTAACCTT | 360 |
| TGGCCTGGAG | GTGTGTTTGG | CCGCAGGCAT | CACCTATGTG | CCGCCTCTGC | TGCTGGAAGT | 420 |
| GGGGTAGAG | GAGAAGTTCA | TGACCATGGT | GCTGGGCATT | GGTCCAGTGC | TGGGCTGGT | 480 |
| CTGTGTCCTCG | CTCCTAGGCT | CAGCCAGTGA | CCACTGGCGT | GGACGCTATG | GCCGCCGCCG | 540 |
| GCCCCTCATC | TGGGCACTGT | CCTTGGGCAT | CCTGCTGAGC | CTCTTCTCA | TCCCAAGGGC | 600 |
| CGGCTGGCTA | GCAGGGCTGC | TGTGCCCGGA | TCCCAGGCC | CTGGAGCTGG | CACTGCTCAT | 660 |
| CCTGGGCGTG | GGGCTGCTGG | ACTTCTGTGG | CCAGGTGTGC | TTCACTCCAC | TGGAGGCCCT | 720 |
| GCTCTCTGAC | CTCTTCCGGG | ACCCGGACCA | CTGTCGCCAG | GCCTACTCTG | TCTATGCCCT | 780 |
| CATGATCAGT | CTTGGGGGCT | GCCTGGCTA | CCTCCTGCCT | GCCATTGACT | GGGACACCAG | 840 |
| TGCCCTGGCC | CCCTACCTGG | GCACCCAGGA | GGAGTGCCTC | TTTGGCCTGC | TCACCCCTCAT | 900 |
| CTTCCTCACC | TGCGTAGCAG | CCACACTGCT | GGTGGCTGAG | GAGGCAGCGC | TGGGCCCCAC | 960 |
| CGAGCCAGCA | GAAGGGCTGT | CGGCCCCCTC | CTTGTGCGCC | CACTGCTGTC | CATGCCGGGC | 1020 |
| CCGCTTGGCT | TTCCGGAACC | TGGGCGCCCT | GCTTCCCCGG | CTGCACCAGC | TGTGCTGCCG | 1080 |
| CATGCCCGC | ACCCCTGCC | GGCTCTTCGT | GGCTGAGCTG | TGCAGCTGG | TGGCACTCAT | 1140 |
| GACCTTCACG | CTGTTTACA | CGGATTCGT | GGGCGAGGGG | CTGTACCAGG | CGTGTGCCAG | 1200 |
| AGCTGAGCCG | GGCACCGAGG | CCCAGGACA | CTATGATGAA | GGCGTTCCGA | TGGGAGCCT | 1260 |
| GGGGCTGTTG | CTGCAGTGCG | CCATCTCCCT | GGTCTTCTCT | CTGGTCATGG | ACCGGCTGGT | 1320 |
| GCAGCGATTC | GGCACTCGAG | CAGTCTATT | GGCCAGTGTG | GCAGCTTCC | CTGTGGCTGC | 1380 |
| CGGTGCCACA | TGCCTGTCCC | ACAGTGTGGC | CGTGGTACA | GCTTCAGCCG | CCCTCACCGG | 1440 |
| GTTCACCTTC | TCAGCCCTGC | AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | 1500 |
| GAAGCAGGTG | TTCCCTGCCCA | AATACCGAGG | GGACACTGGA | GGTGTAGCA | GTGAGGACAG | 1560 |
| CCTGATGACC | AGCTTCTGTC | CAGGCCCTAA | GCCTGGAGCT | CCCTTCCCTA | ATGGACACGT | 1620 |
| GGGTGCTGGA | GGCAGTGGCC | TGCTCCCACC | TCCACCCCGC | CTCTGCGGGG | CCTCTGCCCTG | 1680 |
| TGATGTCTCC | GTACGTGTGG | TGGTGGGTGA | GCCCACCGAG | GCCAGGGTGG | TTCCGGGCCG | 1740 |
| GGGCATCTGC | CTGGACCTCG | CCATCCTGGA | TAGTGCCTTC | CTGCTGTCCC | AGGTGGCCCC | 1800 |
| ATCCCTGTTT | ATGGGCTCCA | TTGTCCAGCT | CAGCCAGTCT | GTCACTGCC | ATATGGTGTG | 1860 |
| TGCCGCAGGC | CTGGGTCTGG | TCGCCATTAA | CTTGTGCTACA | CAGGTAGTAT | TTGACAAGAG | 1920 |
| CGACTTGGCC | AAATACTCAG | CGTAGAAAAC | TTCCAGCACA | TTGGGGTGG | GGGCCTGCCT | 1980 |
| CACTGGGTCC | CAGCTCCCCG | CTCCCTGTTAG | CCCCATGGGG | CTGCCGGGCT | GGCCGCCAGT | 2040 |
| TTCTGTTGCT | GCCAAAGTAA | TGTGGCTCTC | TGCTGCCACC | CTGTGCTGCT | GAGGTGCGTA | 2100 |
| GCTGCACAGC | TGGGGGCTGG | GGCAGTCCCTC | TCCCTCTCTCC | CCAGTCTCTA | GGGCTGCC | 2160 |
| ACTGGAGGCC | TTCCAAGGGGG | GTTCAGTCT | GGACTTATAC | AGGGAGGCCA | GAAGGGCTCC | 2220 |
| ATGCACTGGA | ATGCGGGGAC | TCTGCAGGTG | GATTACCCAG | GCTCAGGGTT | AACAGCTAGC | 2280 |
| CTCCTAGTTG | AGACACACT | AGAGAAGGGT | TTTTGGGAGC | TGAATAAACT | CAGTCACCTG | 2340 |
| GTTTCCCAC | TCTAAGCCCC | TTAACCTGCA | GCTTCGTTTA | ATGTAGCTCT | TGCATGGGAG | 2400 |
| TTTCTAGGAT | GAAACACTCC | TCCATGGGAT | TTGAACATAT | GACTTATTG | TAGGGGAAGA | 2460 |

| | |
|---|------|
| GTCCTGAGGG GCAACACACA AGAACCGAGT CCCCTCAGCC CACAGCACTG TCTTTTGCT | 2520 |
| GATCCACCCC CCTCTTACCT TTTATCAGGA TGTCGGCTGT TGGTCCTCT GTGCCATCA | 2580 |
| CAGAGACACA GGCATTTAAA TATTTAACTT ATTATTTAA CAAAGTAGAA GGGATCCAT | 2640 |
| TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA | 2700 |
| GGTCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTCTT CTCTGGGGT | 2760 |
| CTGGCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTCT TACTCATCCC AAAATGATAAT | 2820 |
| TCCAAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT | 2880 |
| CTCAACGGCT TCCCTAACCA CCCCTCTCT CTTGGCCAG CCGGTTCCC CCCACTTCCA | 2940 |
| CTCCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCTACC | 3000 |
| CCCAACTTTCC CCCCACCCCC AACTTTCCCC ACCAGCTCCA CAACCCCTGTT TGGAGCTACT | 3060 |
| GCAGGACCAAG AAGCACAAG TGCAGTTCC CAAGCCTTTC TCCATCTCAG CCCCCAGAGT | 3120 |
| ATATCTGTGC TTGGGAAATC TCACACAGAA ACTCAGGAGC ACCCCCCTGCC TGAGCTAAGG | 3180 |
| GAGGTCTTAT CTCTCAGGGG GGGTTAACGT CCCGTTGCA ATAATGTCGT CTTATTTATT | 3240 |
| TAGCGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA | 3300 |
| AAATTAAGG CTTCTTATA TGTTAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA | 3360 |
| AAAAAAAARA AAAAAAAA AAAAAAATAA AAAAAAAA | 3410 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|--|------|
| AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCTTT | 60 |
| GTGGAGCCTC AGCAGTTCCC TCTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA | 120 |
| CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTTC | 180 |
| TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCCTTC | 240 |
| TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC | 300 |
| TCATCGCAGC CGGCAGTTGTG GTCTTGCTC TTGGTTTCCCT GGGCTGCTAT GGTGCTAAGA | 360 |
| CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG | 420 |
| AGGTTGCAGC TGCTGTGGTC GCCTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT | 480 |
| TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT | 540 |
| GGAACACCAC CATGAAAGGG CTCAAGTGCT GTGGCTTCAC CAACTATACG GATTTGAGG | 600 |
| ACTCACCCCTA CTTCAAAGAG AACAGTGCT TTCCCCCATT CTGTTGCAAT GACAACGTCA | 660 |
| CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT | 720 |
| GCTTCAATCA GCTTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG | 780 |
| CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC | 840 |
| TACAATAAGT CCACTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACCT GTGAAGAGGC | 900 |
| ACCCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA | 960 |
| GAATGGACCT GCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTAGCG | 1020 |
| ATGCCCTGACT TTCCCTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCAG AGCCTCTAAAG | 1080 |
| GTAGCCAGTT CTGTTGCCA TTCCCCCAGT CTATTAACCC CTTGATATGC CCCCTAGGCC | 1140 |
| TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGGCAT | 1200 |
| AAAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC | 1260 |
| TGTTACAATG TTAAAAAAA AAAAAAAA | 1289 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

| | | |
|---|-----|-----|
| 210 | 215 | 220 |
| Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp | | |
| 225 | 230 | 235 |
| Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val | | |
| 245 | 250 | 255 |
| Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg | | |
| 260 | 265 | 270 |
| Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly | | |
| 275 | 280 | 285 |
| Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly | | |
| 290 | 295 | 300 |
| Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp | | |
| 305 | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | | |
|---|---|----|
| Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala | | |
| 1 | 5 | 10 |
| | | 15 |

| | | |
|---|----|----|
| Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val | | |
| 35 | 40 | 45 |

| | | |
|---|----|----|
| Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly | | |
| 50 | 55 | 60 |

| | | |
|---|----|----|
| Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly | | |
| 65 | 70 | 75 |
| | | 80 |

| | | |
|---|----|----|
| Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile | | |
| 85 | 90 | 95 |

| | | |
|---|-----|-----|
| Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu | | |
| 100 | 105 | 110 |

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

| 50 | 55 | 60 | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Phe | Ala | Leu | Gly | Phe | Leu | Gly | Cys | Tyr | Gly | Ala | Lys | Thr |
| 65 | | | | | 70 | | | | 75 | | | | 80 | | |
| Glu | Ser | Lys | Cys | Ala | Leu | Val | Thr | Phe | Phe | Phe | Ile | Leu | Leu | Ile | |
| | | | | | 85 | | | | 90 | | | | 95 | | |
| Phe | Ile | Ala | Glu | Val | Ala | Ala | Val | Val | Ala | Leu | Val | Tyr | Thr | Thr | |
| | | | | | 100 | | | 105 | | | | 110 | | | |
| Met | Ala | Glu | His | Phe | Leu | Thr | Leu | Leu | Val | Val | Pro | Ala | Ile | Lys | Lys |
| | | | | | 115 | | | 120 | | | | 125 | | | |
| Asp | Tyr | Gly | Ser | Gln | Glu | Asp | Phe | Thr | Gln | Val | Trp | Asn | Thr | Thr | Met |
| | | | | | 130 | | | 135 | | | 140 | | | | |
| Lys | Gly | Leu | Lys | Cys | Cys | Gly | Phe | Thr | Asn | Tyr | Thr | Asp | Phe | Glu | Asp |
| | | | | | 145 | | | 150 | | | 155 | | | 160 | |
| Ser | Pro | Tyr | Phe | Lys | Glu | Asn | Ser | Ala | Phe | Pro | Pro | Phe | Cys | Cys | Asn |
| | | | | | 165 | | | 170 | | | | 175 | | | |
| Asp | Asn | Val | Thr | Asn | Thr | Ala | Asn | Glu | Thr | Cys | Thr | Lys | Gln | Lys | Ala |
| | | | | | 180 | | | 185 | | | | 190 | | | |
| His | Asp | Gln | Lys | Val | Glu | Gly | Cys | Phe | Asn | Gln | Leu | Leu | Tyr | Asp | Ile |
| | | | | | 195 | | | 200 | | | | 205 | | | |
| Arg | Thr | Asn | Ala | Val | Thr | Val | Gly | Gly | Val | Ala | Ala | Gly | Ile | Gly | Gly |
| | | | | | 210 | | | 215 | | | | 220 | | | |
| Leu | Glu | Leu | Ala | Ala | Met | Ile | Val | Ser | Met | Tyr | Leu | Tyr | Cys | Asn | Leu |
| | | | | | 225 | | | 230 | | | | 235 | | | 240 |
| Gln | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | |
|---|-----|
| GCTCTTCCTC TCCCCTCCTC TGAATTAAAT TCTTTCAACT TGCAATTGCA AAGGATTACA | 60 |
| CATTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAA GTGCTTTGT TTAAAATTAC | 120 |
| TTGGTTGTG AATCCATCTT GCTTTTCCC CATTGGAAC TGCAATTAAAC CCATCTCTGA | 180 |
| ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT | 240 |
| TCTCAGAACC ATTCACCCA GACAGCCTGT TTCTATCCTG TTTAATAAAT TAGTTGGGT | 300 |
| TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTCACAT AAAAGTCTGT GACTTGAAGT | 360 |
| TTAGTC | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|---|-----|
| ACAAAGATGA ACCATTTCT ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT | 60 |
| GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA | 120 |
| AGACTTTACT ATTTTCATAT TTTAACACAC ATGATTATC CTATTTAGT AACCTGGTTC | 180 |
| ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTTGGCAGA AAATCTATGT | 240 |
| TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | |
|---|-----|
| ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA | 60 |
| TATTTATCCT CCCTCCTGAA ACAATTGCAA ATAANACAA AATATATGAA ACAATTGCAA | 120 |
| AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA | 180 |
| TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT | 240 |
| GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT | 300 |
| TGGGT | 305 |

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | |
|--|----|
| ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTG CCGCACAAATC TGAGTGGAAA | 60 |
| AANTCCTGGG T | 71 |

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|---|-----|
| ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA | 60 |
| GAAAATGGGG TGAAATTGGC CAACTTCTA TNAACATTATG TTGGCAANTT TGCCACCAAC | 120 |
| AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT | 180 |
| AATGGANTCA AGANACTCCC AGGCCTCAGC GT | 212 |

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|---|----|
| ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC | 60 |
| CTCCGCCGGC GCAGAACATG CTGGGGTGGT | 90 |

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|-----|
| TGTANC GTGA | ANACGACAGA | NAGGGTTGTC | AAAAATGGAG | AAN CCTTGAA | GTCATTTTG | 60 |
| GAATAAGATT | TGCTAAAAGA | TTTGGGGCTA | AAACATGGTT | ATTGGGAGAC | ATTTCTGAAG | 120 |
| ATATNCANGT | AAATTANGGA | ATGAATT CAT | GGTTCTTTG | GGAATTCC TT | TACGATNGCC | 180 |
| AGCATANACT | TCATGTGGGG | ATANCAGCTA | CCCTTGTA | | | 218 |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TAGGGGTGTA | TGCAACTGTA | AGGACAAAAA | TTGAGACTCA | ACTGGCTTAA | CCAATAAAGG | 60 |
| CATTTGTTAG | CTCATGGAAC | AGGAAGTCGG | ATGGTGGGGC | ATCTTCAGTG | CTGCATGAGT | 120 |
| CACCACCCCG | GCGGGGTCA | CTGTGCCACA | GGTCCCTGTT | GACAGTGC | GG | 171 |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| TGTAGCGTGA | AGACNACAGA | ATGGTGTGTG | CTGTGCTATC | CAGGAACACA | TTTATTATCA | 60 |
| TTATCAANTA | TTGTGT | | | | | 76 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

| | |
|--|-----|
| ACCTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT | 60 |
| CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG | 120 |
| TTAAGATTTG T | 131 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | |
|---|-----|
| ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG | 60 |
| CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA | 120 |
| CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTGGAT TAAATGAGGA TGCTGAAGAT | 180 |
| TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAA AAGACAGTGG | 240 |
| CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC | 300 |
| CATGGTGGGG GTCTTGATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG | 360 |
| CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC | 420 |
| CTCTTGCTT GT | 432 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | |
|---|-----|
| ACACAACTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCACT TTCTAACCAT | 60 |
| AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAAATTT GT | 112 |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | |
|---|----|
| ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG | 54 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | |
|---|-----|
| ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCT CTACCAAGCTC | 60 |
| ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA | 120 |
| TTCTCTCTGA AGTCTAGGTT ACCCATTGTT GGGACCCATT ATAGGCAATA AACACAGTTC | 180 |
| CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT | 240 |
| TTCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT | 300 |
| AGGCTGCCTT CTTTCCATG TCC | 323 |

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | |
|--|-----|
| ACATACATGT GTGTATATT TTAAATATCA CTTTGTATC ACTCTGACTT TITAGCATA | 60 |
| TGAAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCAA ATCATTCA | 120 |
| TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCCTCACG TTGGCCAATG | 180 |
| GATAAACAAA GT | 192 |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

| | |
|---|-----|
| CCCTTTTTTA TCCAATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTGACA | 60 |
| TATAATGACG CAACAAAAG GTGCTGTTA GTCTATGGT TCAGTTATG CCCCTGACAA | 120 |
| GTTCCTATTG TGTTTGCCG ATCTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA | 180 |
| TTCTGTATTG CATTGGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA | 240 |
| CTTATTTAAA AGCTTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT | 300 |
| TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTTT GCTAATCTTA AAAAGTAATG | 360 |
| GG | 362 |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | |
|---|-----|
| CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCATGCA | 60 |
| GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA | 120 |
| GTTCTCCAG GTTCGCCCCG CTGCTCCAAG TCTCAGCAGC AGCCTTTTT AGGAGGCATC | 180 |
| TTCTGAAGTA GATTAAGGCA GCTTGAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA | 240 |
| CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGC | 300 |
| ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT | 332 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| ACTTTTGCCA | TTTTGTATAT | ATAAACAAATC | TTGGGACATT | CTCCTGAAAA | CTAGGTGTCC | 60 |
| AGTGGCTAAG | AGAACTCGAT | TTCAAGCAAT | TCTGAAAGGA | AAACCAGCAT | GACACAGAAT | 120 |
| CTCAAATTCC | CAAACAGGGG | CTCTGTGGGA | AAAATGAGGG | AGGACCTTG | TATCTCGGGT | 180 |
| TTTAGCAAGT | TAAAATGAAN | ATGACAGGAA | AGGCTTATT | ATCAACAAAG | AGAAGAGTTG | 240 |
| GGATGCTTCT | AAAAAAAACT | TTGGTAGAGA | AAATAGGAAT | GCTNAATCCT | AGGGAAGCCT | 300 |
| GTAACAATCT | ACAATTGGTC | CA | | | | 322 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| ACAAGCCTTC | ACAAGTTAA | CTAAATGGG | ATTAATCTT | CTGTANTTAT | CTGCATAATT | 60 |
| CTTGTTTTTC | TTTCCATCTG | GCTCCTGGGT | TGACAATTG | TGGAAACAAC | TCTATTGCTA | 120 |
| CTATTTAAAA | AAAATCACAA | ATCTTCCCT | TTAAGCTATG | TTNAATTCAA | ACTATTCCCTG | 180 |
| CTATTCCTGT | TTTGTCAAAG | AAATTATATT | TTTCAAAATA | TGTNTATTG | TTTGATGGGT | 240 |
| CCCACGAAAC | ACTAATAAAA | ACCAACAGAGA | CCAGCCTG | | | 278 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

| | |
|---|-----|
| GT TTANAAAA CTTGTTAGC TCCATAGAGG AAAGAATGTT AAACTTGTA TTTAAAACA | 60 |
| TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTT TACTTGTATT TTGCTTTGG | 120 |
| T | 121 |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | |
|--|-----|
| ACTTANAACC ATGCCTAGCA CATCAGAAC CCTCAAAGAA CATCAGTATA ATCCTATACC | 60 |
| ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCAAG CTGGCACATT ACTTGTGTGC | 120 |
| AAACTTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCCTAGGAN TGGTACTCCA | 180 |
| GGGTGCCCCC CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTCGCT | 240 |
| CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG | 300 |
| TTCCAAGGA TGCAAAGCCT GGTGCTAAC TCCGGGGCG TCAACTCAGT | 350 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | |
|---|-----|
| TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT | 60 |
| GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT | 120 |
| GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA | 180 |
| CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAAONCCAAG | 240 |
| AAAACTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC | 300 |
| TCCCAAGGAAC CGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG | 360 |
| GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT | 399 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | |
|---|-----|
| ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT | 60 |
| GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTTGGCC GTGCTAAATG AGCTTCGGGA | 120 |
| TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT | 165 |

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | |
|---|-----|
| ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC | 60 |
| TTAACTTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA | 120 |
| TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG | 180 |
| TCATGTGTTT CCAGGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGG CATANANGGT | 240 |
| CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTGCCAC TGTACATTCC CCATNTTTAA | 300 |
| AAAAACTGAT GCCTTTTTTG TTTTTTTTG TAAAATTC | 338 |

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | |
|---|-----|
| GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA | 60 |
| GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT AGTGCCGAA GTGAAGGAGA | 120 |
| ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC | 180 |

100

| | |
|---|-----|
| ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG | 240 |
| CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT | 300 |
| GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG | 360 |
| GCCTGGAAC TGTAAAGT GT | 382 |

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|---|-----|
| ACCAAANCTT CTTTCTGTTG TGTTNGATT TACTATAGGG GTTTNGCTTN TTCTAAANAT | 60 |
| ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG | 120 |
| TTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTTT | 180 |
| ATATTCAAGCA TAAAGGAGAA | 200 |

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|--|-----|
| ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAATAA AGTTTGGTGG | 60 |
| GGGTGCTGAC TAAACCTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT | 120 |
| ATGCATGTAG AGAACCCAAA CTAATTATT AAAACAGGATA GAAACAGGCT GTCTGGGTGA | 180 |
| AATGGTTCTG AGAACCATCC AATTACACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG | 240 |
| TTTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG | 300 |
| ATTACAAAC CAAGTAATT TAAACAAAGA CACTT | 335 |

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|--|-----|
| ACCAAGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAACAGA CGTGTATTTA | 60 |
| GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTT CATGGAGTAT | 120 |
| CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA | 180 |
| CACATGGTCC ACAACACCTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC | 240 |
| TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA | 300 |
| TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA | 360 |
| AGCTACCACT AGCTACCACT TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT | 420 |
| CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT | 459 |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|--|-----|
| ACATTTCCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG | 60 |
| AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG | 120 |
| ACCATCCGAC TTCCCTGTGT | 140 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|---|-----|
| ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT | 60 |
| ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTTG | 120 |
| AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT | 164 |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| ACGTAGACCA TCCAACTTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA | 60 |
| ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT | 120 |
| GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAAACTTCA | 180 |
| GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG | 240 |
| TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT | 300 |
| CAA | 303 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC | 60 |
| ACTGCCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTTGC CAACAGGCCT | 120 |
| CCAAGTCAGG GCTGGGATTTC GTTCCCTTTTC CACATTCTAG CAACAATATG CTGGCCACTT | 180 |
| CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTTC TAAAGTAGCC | 240 |
| AGACTTGCCTTCTGGGCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG | 300 |
| TAGGGGTGAG CTGTGTGACT CTATGGT | 327 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|--|-----|
| ACATTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT | 173 |

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|---|-----|
| ACAACCAC TTATCTCATCG AATTTTAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT | 60 |
| ATGGGATATA TTATTTGATG CTCCATTTCATC TCACACATAT ATGAATAATA CACTCATACT | 120 |
| GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG | 180 |
| GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC | 240 |
| NCCANCCAC CTCACCGACC CCATCCCTT ACACAGCTAC CTCCCTGCTC TCTAACCCCCA | 300 |
| TAGATTATNT CCAAATTTCAG TCAATTAAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG | 360 |
| CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT | 420 |
| CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTTAA TTACCATGCT ATGGTGG | 477 |

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAAGAAC | 60 |
| TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT | 120 |
| GATGATAAAAT AAGAGTCAGC CAGGTAAAGTG GGTGGGTGTGG TATGGGCACA GTGAAGAACAA | 180 |
| TTTCAGGCAG AGGGAACAGC AGTGAAA | 207 |

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

| | |
|---|-----|
| ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG | 60 |
| CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGAG T | 111 |

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

| | |
|---|-----|
| AGCGCGGCAG GTCATATTGA ACATTCAGA TACCTATCAT TACTCGATGC TGTTGATAAC | 60 |
| AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT | 120 |
| GGATACCAAC CGGAAACCCC CTATCCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG | 180 |
| GTGCATCCGG CTCAGT | 196 |

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | |
|---|-----|
| ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC | 60 |
| CTTCCCTTT TCATCTAGTG GTGGAACCT GATGCTTAT GTTGACAGGA ATAGAACAG | 120 |
| GAGGGAGTTT GT | 132 |

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | | | |
|---|-----------------------|-----------------------|-----|
| ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCA | TGCC | TCCAAACATG AAAGTGTCA | 60 |
| CTTCTGCTCT TATGTCTCA TCTGACA | ACT CTTTAC | TTTATCCTCG CTCAGCAGGA | 120 |
| GCACATCAAT AAAGTCCAAA GTCTGGACT TGGC | TTGGAGGAAG TCATCAACAC | 180 | |
| CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC | ATCTGTGAAG TCGTGCACCA | 240 | |
| GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG | GAATT | 285 | |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | |
|---|-----|
| ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC | 60 |
| ACCCCAAATT TTTCTTAAAT ATCTTTAAC TGAAGGGGTC AGCCTTGA CTGCAAAGAC | 120 |
| CCTAACCGG TTACACAGCT AACTCCCCT GGCCCTGATT TGTGAAATTG CTGCTGCCTG | 180 |
| ATTGGCACAG GAGTCGAAGG TGTTCAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTTG | 240 |
| AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG | 300 |
| GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG | 333 |

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG | 60 |
| GAAAGTGCCTT TGGGAACGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT | 120 |
| TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC | 180 |
| ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTGGCT | 240 |
| GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AAGCATGCTG | 300 |
| GCCCTGGT | 308 |

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

| | |
|--|-----|
| ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA | 60 |
| TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACGTGA | 120 |
| GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCT CATTCTATGT | 180 |
| CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT | 240 |
| AAAACCAGAT GTCTATCCTT AAGATTTC AATAGAAAAC AAATTAACAG ACTAT | 295 |

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|--|-----|
| ACAAGTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT | 60 |
| GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC | 120 |
| CTTAGT | 126 |

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| ACCCACTGGT | CTTGGAAACA | CCCATCCTTA | ATACGATGAT | TTTTCTGTG | TGTGAAAATG | 60 |
| AANCCAGCAG | GCTGCCCTA | GTCAGTCCTT | CCTTCCAGAG | AAAAAGAGAT | TTGAGAAAGT | 120 |
| GCCTGGTAA | TTCACCATT | ATTTCCTCCC | CCAAACTCTC | TGAGTCCTTC | CTTAATATTT | 180 |
| CTGGTGGTTC | TGACCAAAGC | AGGTCAATGGT | TTGTTGAGCA | TTTGGGATCC | CAGTGAAGTA | 240 |
| NATTTTGTA | GCCTTGATA | CTTAGCCCTT | CCACGCA | AACGGAGTGG | CAGAGTGGT | 300 |
| CCAACCTGT | TTTCCCAGTC | CACGTAGACA | GATTACAGT | GCGGAATTCT | GGAAGCTGGA | 360 |
| NACAGACGGG | CTCTTGCAG | AGCCGGGACT | CTGAGANGGA | CATGAGGGCC | TCTGCCTCTG | 420 |
| TGTTCATTC | CTGATGTCCT | GT | | | | 442 |

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| ACTTCCAGGT | AACGTTGTTG | TTTCCGTTGA | GCCTGAAC | ATGGGTGACG | TTGTAGGTT | 60 |
| TCCAACAAGA | ACTGAGGTTG | CAGAGCGGGT | AGGGAAGAGT | GCTGTTCCAG | TTGCACCTGG | 120 |
| GCTGCTGTGG | ACTGTTGTTG | ATTCCCTCACT | ACGGCCCAAG | GTTGTGGAAC | TGGCANAAAG | 180 |
| GTGTGTTGTT | GGANTTGAGC | TGGGGCGGCT | GTGGTAGGTT | GTGGGCTCTT | CAACAGGGC | 240 |
| TGCTGTGGTG | CCGGGAGNTG | AANGTGTG | GTCACATTGAG | CTTGGCCAGC | TCTGGAAAGT | 300 |
| ANTANATTCT | TCCCTGAAGGC | CAGCGCTTGT | GGAGCTGGCA | NGGGTCANTG | TTGTGTGTA | 360 |
| CGAACCCAGTG | CTGCTGTGGG | TGGGTGTANA | TCCTCCACAA | AGCCTGAAGT | TATGGTGT | 420 |
| TCAGGTAANA | ATGTGGTTTC | AGTGTCCCTG | GGCNGCTGTG | GAAGGTTGTA | NATTGTCACC | 480 |
| AAGGAAATAA | GCTGTGGT | | | | | 498 |

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|-----|
| ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC | 60 |
| AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT | 120 |
| GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC | 180 |
| CACTAGACAT CTICATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC | 240 |
| CCACCCCTAC CTCCATCTCA CACACTGAG CTTTCCACTC TGTATAATTC TAACATCCTG | 300 |
| GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA | 360 |
| CTTGTAGAAT GAAGCCTGGA | 380 |

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

| | |
|--|-----|
| ACTCCACATC CCCTCTGAGC AGGCCGTTGT CGTTCAAGGT GTATTTGCC TTGCCTGTCA | 60 |
| CACTGTCCAC TGGCCCTTA TCCACTGGT GCTTAATCCC TCGAAAGAGC ATGT | 114 |

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|--|-----|
| ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA | 60 |
| GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAAACCGAGA ACATCCAGTC ATACAGCTT | 120 |
| TGGTGATATA TAACTGGCA ATAACCCAGT CTGGTGATAC ATAAAACCTAC TCACGT | 177 |

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|---|-----|
| CATTATACAGACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC | 60 |
| CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT | 120 |
| CATCAGCGGC ATGATGT | 137 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|---|-----|
| CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA | 60 |
| TGCAATGCAT CATGCTATT CATACCTAAT GAGGGAGTTC CAGGAGATTC AACCAAGGAAA | 120 |
| TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGT | 180 |
| GAGACATGCA CTTGCTACCA AACAGAAATT TCATGTTGCA CCCTGTTTC TACACCTGTG | 240 |
| GGTTATGACA AAGACAACTG CCAAAGAACATC TTCAAGAAGG AGGACTGCAA GTATATCGTG | 300 |
| GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT | 360 |
| TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT | 420 |
| GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT | 469 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|---|-----|
| ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG | 60 |
| ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC | 120 |
| TGCAGGCCGC CGGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT | 180 |
| TCCTCTGAGA TGAGT | 195 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|---|-----|
| ACATCTTAGT AGTGTGGCAC ATCAGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC | 60 |
| CGAGGGTCGGA GTCCACACCA CCGGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT | 120 |
| TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT | 180 |
| TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG | 240 |
| GATGCCAACC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC | 300 |
| GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT | 360 |
| NGGGGCCTTT TTGGTGAAC TTC | 383 |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|--|-----|
| ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT | 60 |
| TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC | 120 |
| TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC | 180 |
| TCAAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC | 240 |
| TGANGTC | 247 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | |
|--|-----|
| ACTTCTAAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA | 60 |
| AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG | 120 |
| GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC | 180 |
| AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG | 240 |
| AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA | 273 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

| | |
|--|-----|
| ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC | 60 |
| AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA | 120 |
| CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG | 180 |
| GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC | 240 |
| CTTGCCATGG GCAAAGGCC C TACCACAAA ACAAATAGGA TCACTGCTGG GCACCAGCTC | 300 |
| ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG | 360 |
| AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC | 420 |
| TCGAACACTG A | 431 |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|--|-----|
| ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC | 60 |
| TCAAGGAGCT CTGCAGGCAT TTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT | 120 |
| CCCCGCTAGA AAGACACCCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT | 180 |
| GTATACTTGTC CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT | 240 |
| TCAAAGCTAG GGGTCTGGCA GGTGGA | 266 |

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| GGCAGCCAAA | TCATAAACGG | CGAGGACTGC | AGCCCCCACT | CGCAGCCCTG | GCAGGGGGCA | 60 |
| CTGGTCATGG | AAAACGAATT | GTTCTCTCG | GGCGTCTCTGG | TGCATCCGCA | GTGGGTGCTG | 120 |
| TCAGCCGAC | ACTGTTCCA | GAAGTGAGTG | CAGAGCTCT | ACACCATCGG | GCTGGGCTG | 180 |
| CACAGTCTTG | AGGCCGACCA | AGAGCCAGGG | AGCCAGATGG | TGGAGGCCAG | CCTCTCCGTA | 240 |
| CGGCACCCAG | AGTACAACAG | ACCCTTGCTC | GCTAACGACC | TCATGCTCAT | CAAGTTGGAC | 300 |
| GAATCCGTGT | CCGAGTCTGA | CACCATCCGG | AGCATCAGCA | TTGCTTCGCA | GTGCCCTACC | 360 |
| GCGGGGAACT | CTTGGCTCGT | TTCTGGCTGG | GGTCTGCTGG | CGAACGGCAG | AATGCCCTACC | 420 |
| GTGCTGCAGT | GCGTGAACGT | GTCGGTGGTG | TCTGAGGAGG | TCTGCACTAA | GCTCTATGAC | 480 |
| CCGCTGTACC | ACCCCAGCAT | GTTCCTGCGCC | GGCGGAGGGC | AAGACCAGAA | GGACTCCCTGC | 540 |
| AAACGGTGA | CTGGGGGGCC | CCTGATCTGC | AAACGGTACT | TGCAGGGCCT | TGTGTCTTTC | 600 |
| GGAAAAGCCC | CGTGTGGCCA | AGTTGGCGTG | CCAGGTGTCT | ACACCAACCT | CTGCAAATT | 660 |
| ACTGAGTGG | TAGAGAAAAC | CGTCCAGGGCC | AGTTAACTCT | GGGGACTGGG | AAACCCATGAA | 720 |
| ATTGACCCCC | AAATACATCC | TGCGGAAGGA | ATTCAAGGAAT | ATCTGTTCCC | AGCCCCCTCCT | 780 |
| CCCTCAGGCC | CAGGAGTCCA | GGCCCCCAGC | CCCTCCTCCC | TCAAACCAAG | GGTACAGATC | 840 |
| CCCAGCCCC | CCTCCCTCAG | ACCCAGGAGT | CCAGACCCCC | CAGCCCCCTCC | TCCCTCAGAC | 900 |
| CCAGGAGTCC | AGCCCCCTCCT | CCCTCAGACC | CAGGAGTCCA | GACCCCCCAG | CCCCTCCTCC | 960 |
| CTCAGACCCA | GGGGTCCAGG | CCCCCAACCC | CTCCTCCCTC | AGACTCAGAG | GTCCAAGGCC | 1020 |
| CCAACCCNTC | ATTCCCCAGA | CCCAGAGGTC | CAGGTCCCTAG | CCCTCTCCTCC | CTCAGACCCA | 1080 |
| GCGGTCCAAT | GCCACCTAGA | CTNTCCCTGT | ACACAGTGCC | CCCTTGTGGC | ACGTTGACCC | 1140 |
| AACCTTACCA | GTTGGTTTTT | CATTTTTNGT | CCCTTCCCC | TAGATCCAGA | AATAAAGTT | 1200 |
| AAGAGAAGNG | AAAAAAAAAA | AAAAAAAAAA | AAAAAAAAAA | AAAAAAA | | 1248 |

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95

Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110

Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125

Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

| | |
|---|-----|
| GGCAGCCCGC ACTCGCAGCC CTGGCAGCG GCACGGTCA TGGAAACGA ATTGTTCTGC | 60 |
| TCGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTT CCAGAACTCC | 120 |
| TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG | 180 |
| GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCCTGCT CGCTAACGAC | 240 |
| CTCATGCTCA TCAAGTTGGA CGAACCCGTG TCCGAGTCTG ACACCATCCG GAGCATCAGC | 300 |
| ATTGCTTCGC AGTGCCCTAC CGCGGGGAAC TCTTGCCTCG TTTCTGGCTG GGGCTTGCTG | 360 |
| GCGAACGGTG AGCTCACGGG TGTGTGCTG CCCTCTCAA GGAGGTCCCTC TGCCCAGTCG | 420 |
| CGGGGGCTGA CCCAGAGCTC TGCCTCCAG GCAGAAATGCC TACCGTGCTG CAGTGCCTGA | 480 |
| ACGTGTCGGT GGTGTCTGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCAACCCA | 540 |
| GCATGTTCTG CGCCGGCGGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG | 600 |
| GGCCCTGTAT CTGCAACGGG TACTTGCAGG GCCTTGTGTC TTTCGGAAAA GCCCCGTGTG | 660 |
| GCCAAGTTGG CGTGCACCCA ACCTCTGCAA ATTCACTGAG TGGATAGAGA | 720 |

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| AAACCGTCCA | GGCCAGTTAA | CTCTGGGAC | TGGGAACCCA | TGAAATTGAC | CCCCAAATAC | 780 |
| ATCCTGCGGA | AGGAATTCTAG | GAATATCTGT | TCCCAGCCCC | TCCTCCCTCA | GGCCAGGAG | 840 |
| TCCAGGCCCC | CAGCCCCCTCC | TCCCTCAAAC | CAAGGGTACA | GATCCCCAGC | CCCTCCCTCCC | 900 |
| TCAGACCCAG | GAGTCCAGAC | CCCCCAGCCC | CTCCTCCCTC | AGACCCAGGA | GTCCAGCCCC | 960 |
| TCCTCCNTCA | GACCCAGGAG | TCCAGACCCC | CCAGCCCCCTC | CTCCCTCAGA | CCCAGGGTT | 1020 |
| GAGGCCCCCA | ACCCCTCCTC | CTTCAGAGTC | AGAGGTCCAA | GCCCCCAACC | CCTCGTTCCC | 1080 |
| CAGACCCAGA | GTNNNAGGTC | CCAGCCCCCTC | TTCCNTCAGA | CCCAGNGGTC | CAATGCCACC | 1140 |
| TAGATTTTCC | CTGNACACAG | TGCCCCCTTG | TGGNANGTTG | ACCCAACCTT | ACCAGTTGGT | 1200 |
| TTTTCATTTT | TNGTCCCTTT | CCCCTAGATC | CAGAAATAAA | GTTTAAGAGA | NGNGAAAAAA | 1260 |
| AAAAAA | | | | | | 1265 |

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|------|
| GGTCAGCCGC | ACACTGTTTC | CAGAAGTGAG | TGCAGAGCTC | CTACACCATC | GGGCTGGGCC | 60 |
| TGCACAGTCT | TGAGGCCGAC | CAAGAGCCAG | GGAGGCCAGAT | GGTGGAGGCC | AGCCTCTCCG | 120 |
| TACGGCACCC | AGAGTACAAC | AGACCCCTTG | TCGCTAACGA | CCTCATGCTC | ATCAAGTTGG | 180 |
| ACGAATCCGT | GTCCGAGTCT | GACACCATCC | GGAGCATCAG | CATTGCTTCG | CAGTGCCTA | 240 |
| CCGGGGGAA | CTCTTGCCTC | GTTCCTGGCT | GGGGTCTGCT | GGCGAACGGT | GAGCTCACGG | 300 |
| GTGTGTGTCT | GCCCTCTTC | AGGAGGTCT | CTGCCAGTC | GCGGGGGCTG | ACCCAGAGCT | 360 |
| CTGCGTCCCA | GGCAGAATGC | CTACCGTGT | GCAGTGCCTG | AACGTGTCGG | TGGTGTCTGA | 420 |
| NGAGGTCTGC | ANTAAAGCTCT | ATGACCGCT | GTACCAACCCC | ANCATGTTCT | GCGCCGGCGG | 480 |
| AGGGCAAGAC | CAGAAGGACT | CCTGCAACGT | GAGAGAGGGG | AAAGGGGAGG | GCAGGCGACT | 540 |
| CAGGGAAGGG | TGGAGAAGGG | GGAGACAGAG | ACACACAGGG | CCGCATGGCG | AGATGCAGAG | 600 |
| ATGGAGAGAC | ACACAGGGAG | ACAGTGACAA | CTAGAGAGAG | AAACTGAGAG | AAACAGAGAA | 660 |
| ATAAACACAG | GAATAAAAGAG | AAGCAAAGGA | AGAGAGAAAC | AGAAACAGAC | ATGGGGAGGC | 720 |
| AGAAACACAC | ACACATAGAA | ATGCAGTTGA | CCTTCCAACA | GCATGGGGCC | TGAGGGCGGT | 780 |
| GACCTCCACC | CAATAGAAAA | TCCTCTTATA | ACTTTTGACT | CCCCAAAAC | CTGACTAGAA | 840 |
| ATAGCCTACT | GTTGACGGGG | AGCCTTACCA | ATAACATAAA | TAGTCGATTT | ATGCATACGT | 900 |
| TTTATGCATT | CATGATATAC | CTTTGTTGGA | ATTTTTGAT | ATTTCTAAGC | TACACAGTTC | 960 |
| GTCTGTGAAT | TTTTTTAAAT | TGTTGCAACT | CTCCTAAAAT | TTTCTGATG | TGTTTATTGA | 1020 |
| AAAAATCCAA | GTATAAGTGG | ACTTGTGCAT | TCAAACCCAGG | GTTGTTCAAG | GGTCAACTGT | 1080 |
| GTACCCAGAG | GGAAACAGTG | ACACAGATTC | ATAGAGGTGA | AACACGAAGA | GAAACAGGAA | 1140 |
| AAATCAAGAC | TCTACAAAGA | GGCTGGGCAG | GGTGGCTCAT | GCCTGTAATC | CCAGCACTTT | 1200 |
| GGGAGGGCAG | GCAGGCAGAT | CACTTGAGGT | AAGGAGTTCA | AGACCAGCCT | GGCCAAAATG | 1260 |
| GTGAAATCCT | GTCTGTACTA | AAAATACAAA | AGTTAGCTGG | ATATGGTGGC | AGGCCTGT | 1320 |
| AATCCCAGCT | ACTTGGGAGG | CTGAGGCAGG | AGAATTGCTT | GAATATGGGA | GGCAGAGGTT | 1380 |
| GAAGTGAGTT | GAGATCACAC | CACTATACTC | CAGCTGGGGC | AACAGAGTAA | GACTCTGTCT | 1440 |
| CAAAAAAAA | AAAAAAA | | | | | 1459 |

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| GGCGAGCCCT | GGCAGGCGGC | ACTGGTCATG | GAAAACGAAT | TGTTCTGCTC | GGGCGTCCTG | 60 |
| GTGCATCCGC | AGTGGGTGCT | GTCAGCCGCA | CACTGTTTCC | AGAACTCCTA | CACCATCGGG | 120 |
| CTGGGCCTGC | ACAGTCTTGA | GGCCGACCAA | GAGCCAGGGA | GCCAGATGGT | GGAGGCCAGC | 180 |
| CTCTCCGTAC | GGCACCCAGA | GTACAAACAGA | CTCTTGCTCG | CTAACGACCT | CATGCTCATC | 240 |
| AAGTGGACG | AATCCGTGTC | CGAGTCTGAC | ACCATCCGGA | GCATCAGCAT | TGCTTCGCAG | 300 |
| TGCCCTACCG | CGGGGAACTC | TTGCCTCGTN | TCTGGCTGGG | GTCTGCTGGC | GAACGGCAGA | 360 |
| ATGCCTACCG | TGCTGCACTG | CGTGAACTGT | TGGGTGGTGT | CTGAGGANGT | CTGCAGTAAG | 420 |
| CTCTATGACC | CGCTGTACCA | CCCCAGCATG | TTCTGCGCCG | GCGGAGGGCA | AGACCCAGAAG | 480 |
| GACTCCTGCA | ACGGTGACTC | TGGGGGGCCC | CTGATCTGCA | ACGGGTACTT | GCAGGGCCTT | 540 |
| GTGTCTTCG | GAAAAGCCCC | GTGTGGCCAA | CTTGGCGTGC | CAGGTGTCTA | CACCAACCTC | 600 |
| TGCAAATTCA | CTGAGTGGAT | AGAGAAAACC | GTCCAGNCCA | GTAACTCTG | GGGACTGGGA | 660 |
| ACCCATGAAA | TTGACCCCCA | AATACATCCT | GCGGAANGAA | TTCAGGAATA | TCTGTTCCCA | 720 |
| GCCCCTCCCT | CCTCAGGGCCC | AGGAGTCCAG | GCCCCCAGCC | CCTCCTCCCT | CAAACCAAGG | 780 |
| GTACAGATCC | CCAGCCCCCTC | CTCCCTCAGA | CCCAAGGAGTC | CAGACCCCCC | AGCCCCCTCNT | 840 |
| CCNTCAGACC | CAGGAGTCCA | GCCCCCTCCCT | CNTCAGACGC | AGGAGTCCAG | ACCCCCCAGC | 900 |
| CCNTCNTCCG | TCAGACCCAG | GGGTGCAGGC | CCCCAACCCC | TCNTCCNTCA | GAGTCAGAGG | 960 |
| TCCAAGCCCC | CAACCCCTCG | TTCCCCAGAC | CCAGAGGTNC | AGGTCCCAGC | CCCTCCTCC | 1020 |
| TCAGACCCAG | CGGTCCAATG | CCACCTAGAN | TNTCCCTGTA | CACAGTCCCC | CCTTGTGGCA | 1080 |
| NGTTGACCCA | ACCTTACCAAG | TTGGTTTTTC | ATTTTTGTC | CCTTTCCCT | AGATCCAGAA | 1140 |
| ATAAAGTNTA | AGAGAAGCGC | AAAAAAA | | | | 1167 |

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Leu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1 | | | | 5 | | | | | 10 | | | 15 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Asn | Ser | Tyr | Thr | Ile | Gly | Leu |
| | | | | | 20 | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | His | Ser | Leu | Glu | Ala | Asp | Gln | Glu | Pro | Gly | Ser | Gln | Met | Val |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

35

40

45

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Leu | Leu | Leu |
| 50 | | | | | | | | | | | | | | | |
| Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser | Glu | Ser |
| 65 | | | | | | | | | | | | | | | |
| Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr | Ala | Gly |
| | | | | | | | | | | | | | | | |
| 85 | | | | | | | | | | | | | | | |
| Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Gly | Arg | Met |
| | | | | | | | | | | | | | | | |
| 100 | | | | | | | | | | | | | | | |
| Pro | Thr | Val | Leu | His | Cys | Val | Asn | Val | Ser | Val | Val | Ser | Glu | Xaa | Val |
| | | | | | | | | | | | | | | | |
| 115 | | | | | | | | | | | | | | | |
| Cys | Ser | Lys | Leu | Tyr | Asp | Pro | Leu | Tyr | His | Pro | Ser | Met | Phe | Cys | Ala |
| | | | | | | | | | | | | | | | |
| 130 | | | | | | | | | | | | | | | |
| Gly | Gly | Gly | Gln | Asp | Gln | Lys | Asp | Ser | Cys | Asn | Gly | Asp | Ser | Gly | Gly |
| | | | | | | | | | | | | | | | |
| 145 | | | | | | | | | | | | | | | |
| Pro | Leu | Ile | Cys | Asn | Gly | Tyr | Leu | Gln | Gly | Leu | Val | Ser | Phe | Gly | Lys |
| | | | | | | | | | | | | | | | |
| 165 | | | | | | | | | | | | | | | |
| Ala | Pro | Cys | Gly | Gln | Leu | Gly | Val | Pro | Gly | Val | Tyr | Thr | Asn | Leu | Cys |
| | | | | | | | | | | | | | | | |
| 180 | | | | | | | | | | | | | | | |
| Lys | Phe | Thr | Glu | Trp | Ile | Glu | Lys | Thr | Val | Gln | Xaa | Ser | | | |
| | | | | | | | | | | | | | | | |
| 195 | | | | | | | | | | | | | | | |
| 200 | | | | | | | | | | | | | | | |
| 205 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| GCGCACTCGC | AGCCCTGGCA | GGCGGCACTG | GTCATGGAAA | ACGAATTGTT | CTGCTCGGGC | 60 |
| GTCTCTGGTGC | ATCCGCAGTG | GGTGCTGTCA | GCCGCACACT | GTTTCCAGAA | CTCCTACACC | 120 |
| ATCGGGCTGG | GCCTGCACAG | TCTTGAGGCC | GACCAAGAGC | CAGGGAGCCA | GATGGTGAG | 180 |
| GCCAGCCTCT | CCGTACGGCA | CCCAGAGTAC | AACAGACCC | TGCTCGCTAA | CGACCTCATG | 240 |
| CTCATCAAGT | TGGACGAATC | CGTGTCCGAG | TCTGACACCA | TCCGGAGCAT | CAGCATTGCT | 300 |
| TCGCAGTGCC | CTACCGCGGG | GAACCTTGC | CTCGTTTCTG | GCTGGGGTCT | GCTGGCGAAC | 360 |
| GATGCTGTGA | TTGCCATCCA | GTCCCAGACT | GTGGGAGGCT | GGGAGGTGTGA | GAAGCTTTCC | 420 |
| CAACCCTGGC | AGGGTTGTAC | CATTCGGCA | ACTTCCAGTG | CAAGGACGTC | CTGCTGCATC | 480 |

| | |
|---|------|
| CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG | 540 |
| CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT | 600 |
| ACTAACCATG CCGATGTTA GGTGAAATTG GCGTCACTTG GCCTCAACCA TCTTGGTATC | 660 |
| CAGTTATCCT CACTGAATTG AGATTCCTG CTTCAAGGT GCTGGTACTC CCCTCACAAA | 720 |
| TGACCTACAG AGGTGAGGGG TCATATAGCT CTTCAAGGT GCTGGTACTC CCCTCACAAA | 780 |
| TTCATTTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG TGGGTGTGCA | 840 |
| GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTAA ATCCCTCATG | 900 |
| CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTG CATTGATGCA | 960 |
| ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTGGG | 1020 |
| GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC | 1080 |
| TTAATAAACAA GAAGCTGTGA TGTAAAAAAA AAAAAAAA | 1119 |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Ileu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1 | | | | 5 | | | | | | | | 10 | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Asn | Ser | Tyr | Thr | Ile | Gly | Leu |
| | | | | | | | 20 | | | | | 25 | | | 30 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | His | Ser | Leu | Glu | Ala | Asp | Gln | Glu | Pro | Gly | Ser | Gln | Met | Val |
| | | | | 35 | | | | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro | Leu | Leu |
| | | | | | 50 | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser | Glu | Ser |
| | | | | 65 | | 70 | | | | 75 | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr | Ala | Gly |
| | | | | | 85 | | | | 90 | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Asp | Ala | Val |
| | | | | 100 | | | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Ile | Gln | Ser | Xaa | Thr | Val | Gly | Gly | Trp | Glu | Cys | Glu | Lys | Leu |
| | | | | | 115 | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Pro | Trp | Gln | Gly | Cys | Thr | Ile | Ser | Ala | Thr | Ser | Ser | Ala | Arg |
| | | | | 130 | | 135 | | | 140 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ser | Cys | Cys | Ile | Leu | Thr | Gly | Cys | Ser | Leu | Leu | Thr | Ala | Ser | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|

145

150

155

160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

| | |
|---|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT | 60 |
| CCAGCTGCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGC TGTGATTGCT | 120 |
| GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA | 180 |
| AAGTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAAA | 240 |
| AAAAAAAAAA | 250 |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | |
|--|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACAA | 60 |
| TCACCCAGAC CCCGCCCTG CCCGTGCCCG ACGCTGCTGC TAACGACAGT ATGATGCTTA | 120 |
| CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTGTT TATAATGCC | 180 |
| TGATTTAAAA AAAAAAAAAA AA | 202 |

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | |
|--|-----|
| TCCYTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG | 60 |
| AATGTTAGG CAGTGCTAGT AATTCTYTCG TAATGATTCT GTTATTACTT TCCTNATTCT | 120 |
| TTATTCCCTCT TTCTTCTGAA GATTAATGAA GTTAAAATT GAGGTGGATA AATACAAAAAA | 180 |
| GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA | 240 |
| AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTATAT GCTGTTAAC | 300 |
| CTACTCTGTT CCTTGGCTAG AAAAATTAT AACACAGGACT TTGTTAGTTT GGGAGCCAA | 360 |
| ATTGATAATA TTCTATGTTA TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW | 420 |

| | |
|---|-----|
| TTTTATTCCC AGGAATATGG KGTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT | 480 |
| AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC | 540 |
| CAAAAAAAA AAAAAAAA | 558 |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

| | |
|--|-----|
| ACAGGGWTK GRGGATGCTA AGSCCCCRGA RWTYGTTGA TCCAACCCTG GCTTWTTTTC | 60 |
| AGAGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG | 120 |
| CSTCACACAG ASTCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG | 180 |
| TTWGCAATTG ACGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGTGATG TCCTTAGTCA | 240 |
| CTAAGGTTAA ACTTCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA | 300 |
| TACTMTTCTA AGTCTCTTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT | 360 |
| NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TACGCATARA | 420 |
| AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAA AAAAAAAA AAAAAAAA | 479 |

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | |
|--|-----|
| AGGCAGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC | 60 |
| AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCAGCA CCAGTGGTGG CTTCAGTGCT | 120 |
| GGTGCCAGCC TGACCGCCAC TCTCACATTG GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT | 180 |
| GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTTCTCCT ACAAGTGAGA TTTTAGATAT | 240 |
| TGTTAACCTCTT GCCAGTCTT CTCTTCAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA | 300 |
| CAGCACTCTA GGCAAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT | 360 |
| GCCATTCAA AAAAAAAA AAAA | 384 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

| | |
|---|----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYYNT CCRGTATKAC CTCAACGAGC | 60 |
|---|----|

| | |
|---|-----|
| AGGGAGATCG AGTCTATAACG CTGAAGAAAT TTGACCCGAT GGGACAAACAG ACCTGCTCAG | 120 |
| CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAAC ACCATCAAGA | 180 |
| AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC | 240 |
| TGATGTCTTT TCTGCAACT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG | 300 |
| TGAGCCCTGA TGCCTTTTGT CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCGATTG | 360 |
| ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGGAACAC ATTTGACTTT | 420 |
| TTTTCTCAT ATTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST | 480 |
| TAAAAAAA AAAAAA | 496 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | |
|--|-----|
| GCTGGTAGGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC | 60 |
| CAAGTATCYT GCGCSCGGTC TTCTACCGTC CCTACCTGCA GATCTCGGG CAGATTCCCC | 120 |
| AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT | 180 |
| GGGCACACCCC TCCTGGGGCC CAGGGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG | 240 |
| TGGTGCTGCT CCTCGTCATC TTCCCTGCTCG TGGCAACAT CCTGCTGGTC AACTTGCTCA | 300 |
| TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG | 360 |
| GGCAGCGTT ACCGCCTCAT CCGG | 384 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | |
|--|-----|
| GAGTTAGCTC CTCCACAAACC TTGATGAGGT CGTCTGCAGT GGCCCTCTCGC TTCAACCGC | 60 |
| TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT | 120 |
| CCAGGAAACT CTCAAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTTCCGC | 180 |
| TCCGTGTGAA AGGATCTCCC AGAAGGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT | 240 |
| ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTCAC | 300 |
| CAGCCCTATC ATGCCGTGTA MCGTGCAGA GARCACCGAG CCTTGTGTGG GGGKKGAAGT | 360 |
| CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGCAAAG ACATTGACAA ACTCGCCAG | 420 |
| GTGGAAAAAG AMCAMCTCT GGARGTGTCTN GCGCCTCCTC GTCMGTGGT GGCAGCGCTW | 480 |
| TCCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC | 540 |
| AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT | 577 |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| AACATCTTCC | TGTATAATGC | TGTGTAATAT | CGATCCGATN | TTGTCGSGTG | AGAATYCATW | 60 |
| ACTKGGAAA | GMAACATTAA | AGCCTGGACA | CTGGTATTAA | AATTCAACAT | ATGCAACACT | 120 |
| TTAACACAGTG | TGTCAATCTG | CTCCCYYNAC | TTTGTATCA | CCAGTCTGGG | AAKAAGGGTA | 180 |
| TGCCCTATTG | ACACCTGTTA | AAAGGGCGCT | AAGCATTITTT | GATTCAACAT | CTTTTTTTTT | 240 |
| GACACAAGTC | CGAAAAAAAGC | AAAAGTAAAC | AGTTATYAT | TTGTTAGCCA | ATTCACTTTC | 300 |
| TTCATGGGAC | AGAGCCATYT | GATTAAAAAA | GCAAATTGCA | TAATATTGAG | CTTYGGGAGC | 360 |
| TGATATTGAG | GCGGAAGAGT | AGCCTTCTA | CTTCACCAGA | CACAACCTCCC | TTTCATATTG | 420 |
| GGATGTTNAC | NAAAGTWATG | TCTCTWACAG | ATGGGATGCT | TTTGTCGCAA | TTCTGTTCTG | 480 |
| AGGATCTCCC | AGTTTATTAA | CCACTTGCAC | AAGAAGGCGT | TTTCTTCCTC | AGGC | 534 |

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | | | | | | |
|-------------|------------|------------|-------------|------------|-------------|-----|
| AGAAACCAGT | ATCTCTNAAA | ACAACCTCTC | ATACCTTGTG | GACCTAATT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTT | TACTTTGTA | AAAGCTTATG | 120 |
| CCTCTTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTCAA | TCTAGTTNGT | 240 |
| TTTATTCGAC | ATGAAGGAAA | TTTCCAGATN | ACAACACTNA | CAAACCTCTC | CTKGACKARG | 300 |
| GGGGACAAAG | AAAAGCAAAA | CTGAMCATAA | RAAACATWA | CCTGGTGAGA | ARTTGCATAA | 360 |
| ACAGAAATWR | GGTAGTATAT | TGAARNACAG | CATCATTAAA | RMGTTWTKTT | WTTCCTCCCTT | 420 |
| GCAAAAAACA | TGTACNGACT | TCCCCTTGAG | TAATGCCAAG | TTGTTTTTT | TATNATAAAA | 480 |
| CTTGCCCTTC | ATTACATGTT | TNAAAGTGGT | GTGGTGGGCC | AAAATATTGA | AATGATGGAA | 540 |
| CTGACTGTATA | AAGCTGTACA | AATAAGCAGT | GTGCCTAACAA | AGCAACACAG | TAATGTTGAC | 600 |
| ATGCTTAATT | CACAAATGCT | AATTCTATTA | TAATGTTTG | CTAAATACAA | CTTGAACTA | 660 |
| TTTTTCTGTN | TTCCCAGAGC | TGAGATNTA | GATTTATGT | AGTATNAAGT | AAAAAANTAC | 720 |
| GAAAATAATA | ACATTGAAGA | AAAANANAAA | AAANAAAAAA | A | | 761 |

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTGCCGATN | CTACTATTTT | ATTGCAGGAN | GTGGGGGTGT | ATGCACCGCA | 60 |
| CACCGGGGCT | ATNAGAAGCA | AGAAGGAAGG | AGGGAGGGCA | CAGCCCCCTG | CTGAGCAACA | 120 |
| AAGCCGCCTG | CTGCCTTCTC | TGTCTGTCTC | CTGGTGCAGG | CACATGGGGA | GACCTTCCCC | 180 |

| | |
|---|-----|
| AAGGCAGGGG CCACCAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG | 240 |
| TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCAG | 300 |
| GTCATTGTGC CCTGCCAGG CACAGCGTAN ATCTGGAAA GACAGAATGC TTTCTTTTC | 360 |
| AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTTNG GCTNGGTCTT GGTACNCTTG | 420 |
| GTTCGGCCA GCTCCNCCTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCNGGNCCC | 480 |
| CC | 482 |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | |
|--|-----|
| TTTTTTTTTT TTTTAAACAA GTTTTCACA ACAAAATTAA TTAGAAGAAAT AGTGGTTTTG | 60 |
| AAAACACTCG CATCCAGTGA GAACTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA | 120 |
| AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAAG | 180 |
| CGCTTTGAC ATACAATGCA CAAAAAAAAGGGGGGGGG GACCACATGG ATTAAAATT | 240 |
| TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT | 300 |
| TGAAAAAATT CATGTATGCA ATCCAACCAA AGAAACTTNAT TGGTGATCAT GANTNCTCTA | 360 |
| CTACATCNAC CTTGATCATTT GCCAGGAACN AAAAGTTNAA ANCACNCNGT ACAAAAANAA | 420 |
| TCTGTAATTN ANTTCAACCT CCGTACNGAA AAATNTNNNT TATACACTCC C | 471 |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | |
|--|-----|
| GAGGGATTGA AGGTCTGTTT TASTGTCGGM CTGTTCAGCC ACCAACTCTA ACAAGTTGCT | 60 |
| GTCTTCCACT CACTGTCTGT AAGCTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA | 120 |
| ATTCCTCACC AGTCACATCT TCTAGGACCT TTTTGGATTTC AGTTAGTATA AGCTCTTCCA | 180 |
| CTTCCTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTAGAAAGG AATTYAATTG | 240 |
| CTCGTTCTCT AACAAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC | 300 |
| CTTTGTGCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC | 360 |
| AAGAGTCATC TGTCTGCAAA AGTGCCTTA GTATATCTGC CA | 402 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | | | | | | |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| GAGCTCGGAT | CCAATAATCT | TTGCTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT | 60 |
| GGTCTACCCC | ACATGGGAGC | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC | 120 |
| ATGCCYTYTTT | GAYTACCGTG | TGCCAAGTGC | TGGTGATTCT | YAAACACACYT | CCATCCCGBT | 180 |
| CTTTTGTGGA | AAAACGTGGC | CTTKTCTGGA | ACTAGCARGA | CATCACTTAC | AAATTCAACCC | 240 |
| ACGAGACACT | TGAAAGGTGT | AACAAAGCGA | YTCTTGCATT | GCTTTTGTC | CCTCCGGCAC | 300 |
| CAGTTGTCAA | TACTAACCCG | CTGGTTGCC | TCCATCACAT | TTGTGATCTG | TAGCTCTGGA | 360 |
| TACATCTCCT | GACAGTACTG | AAGAATTCTCT | TCTTTTGTTT | CAAAGCARC | TCTGGTGCC | 420 |
| TGTGATCA | GGTTCCCATT | TCCCAGTCYG | AATGTTCACA | TGGCATATT | WACCTCCAC | 480 |
| AAAACATTGC | GATTTGAGGC | TCAGCAACAG | CAAATCCTGT | TCCGGCATTG | GCTGCAAGAG | 540 |
| CCTCGATGTA | GCCGGCCAGC | GCCAAGGCAG | GCGCCGTGAG | CCCCACCAGC | AGCAGAAAGCA | 600 |
| G | | | | | | 601 |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | | | | | | |
|------------|------------|-------------|-------------|------------|-------------|-----|
| ATACAGCCCA | NATCCCACCA | CGAAAGATGCG | CTTGTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCGCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGGTTGATGC | TGCACTCYTT | 120 |
| CCCAACGCAG | GCAGMAGCGG | GSCCGGTCAA | TGAACCTCCAY | TCGTGGCTTG | GGGTKGACGG | 180 |
| TKAAGTGCAG | GAAGAGGCTG | ACCACCTCGC | GGTCCACCAG | GATGCCCGAC | TGTGCGGGAC | 240 |
| CTGCAGCGAA | ACTCCTCGAT | GGTCATGAGC | GGGAAGCGAA | TGAGGCCAG | GGCCTTGCCC | 300 |
| AGAACCTTCC | GCCTGTTCTC | TGGCGTCACC | TGCAGCTGCT | GCCGCTGACA | CTCGGCCTCG | 360 |
| GACCAGCGGA | CAAACGGCRT | TGAACAGCCG | CACCTCACGG | ATGCCCAGTG | TGTCGCGCTC | 420 |
| CAGGAMMGSC | ACCAGCGTGT | CCAGGTCAAT | GTCGGTGAAG | CCCTCCGCGG | GTRATGGCGT | 480 |
| CTGCAGTGT | TTTGTGATG | TTCTCCAGGC | ACAGGCTGGC | CAGCTGCGGT | TCATCGAAGA | 540 |
| GTCGCGCTG | CGTGAGCAGC | ATGAAGGCAGT | TGTCGGCTCG | CAGTTCTTCT | TCAGGAAACTC | 600 |
| CACGCAAT | | | | | | 608 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| GAACGGCTGG | ACCTTGCCTC | GCATTGTGCT | TGCTGGCAGG | GAATACCTTG | GCAAGCAGYT | 60 |
| CCAGTCCGAG | CAGCCCCAGA | CCGCTGCCGC | CCGAAGCTAA | GCCTGCCTCT | GGCCTTCCCC | 120 |
| TCCGCCTCAA | TGCAGAACCA | GTAGTGGGAG | CACTGTGTTT | AGAGTTAAGA | GTGAACACTG | 180 |
| TTTGATTTA | CTTGGGAATT | TCCTCTGTTA | TATAGCTTTT | CCCAATGCTA | ATTCTCAAAC | 240 |
| AAACAACAACA | AAATAACATG | TTTGCCTGTT | AAAGTTGTATA | AAAGTAGGTG | ATTCTGTATT | 300 |
| TAAAGAAAAT | ATTACTGTTA | CATATACTGC | TTGCAATTTC | TGTATTATT | GKTNCTSTGG | 360 |
| AAATAAAATAT | AGTTATTAAA | GGTTGTCANT | CC | | | 392 |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | | | | | | |
|-------------|-------------|-------------|------------|------------|------------|-----|
| CCSTTKGAGG | GGTKAGGKYC | CAGTTYCCGA | GTGGAAGAAA | CAGGCCAGGA | GAAGTGCCTG | 60 |
| CCGAGCTGAG | GCAGATGTC | CCACAGTGAC | CCCCAGAGCC | STGGGSTATA | GTYTCTGACC | 120 |
| CCTCNCAAGG | AAAGACCACCS | TTCTGGGGAC | ATGGGCTGGA | GGGCAGGACC | TAGAGGCACC | 180 |
| AAGGGAAAGGC | CCCATTCCGG | GGSTGTTCCC | CGAGGAGGAA | GGGAAGGGC | TCTGTGTGCC | 240 |
| CCCCASGAGG | AAGAGGCCCT | GAGTCCTGGG | ATCAGACACC | CCTTCACGTG | TATCCCCACA | 300 |
| CAAATGCAAG | CTCACCAAGG | TCCCCCTCTCA | GTCCCCCTCC | STACACCTG | AMCGGCCACT | 360 |
| GSCSCACACC | CACCCAGAGC | ACGCCACCCG | CCATGGGGAR | TGTGCTAAG | GARTCGCNGG | 420 |
| GCARCGTGG | CATCTNGTCC | CAGAAGGGGG | CAGAATCTCC | AATAGANGGA | CTGARCMSTT | 480 |
| GCTNANAAAAA | AAAAANAAAAA | AA | | | | 502 |

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACCATT | TTGTCCTGCTC | 60 |
| CCTCTGGAAG | CCTTGCAG | AGCGGACTTT | GTAATGTTG | GAGAATAACT | GCTGAATT | 120 |
| WAGCTGTTK | GAGTTGATTS | GCACCACTGC | ACCCACA | TCAATATGAA | AACYAWTTGA | 180 |
| ACTWATTTAT | TATCTTGTGA | AAAGTATAAC | AATGAA | TTGTTCATAC | TGTATTKATC | 240 |
| AAGTATGATG | AAAAGCAAWA | GATATATATT | CTTTTATTAT | GTAAATTAT | GATTGCCATT | 300 |
| ATTAATCGGC | AAAATGTGGA | GTGTATGTC | TTTCACAGT | AATATATGCC | TTTGTA | 360 |
| TCACTTGGTT | ATTTTATTGT | AAATGARTTA | CAAAATTCTT | AATTTAAGAR | AATGGTATGT | 420 |
| WATATTATT | TCATTAATT | CTTTCCTKGT | TTACGTTAAT | TTTGAAGA | WTGCATGATT | 480 |
| TCTTGACAGA | AATCGATCTT | GATGCTGTGG | AAAGTAGTTG | ACCCACATCC | CTATGAGTT | 540 |
| TTCTTGAAT | GTATAAAGGT | TGTAGCCAT | CNAACTTCAA | AGAAAAAAAT | GACCACATAC | 600 |
| TTTGCAATCA | GGCTGAAATG | TGGCATGCTN | TTCTAATTCC | AACTTTATAA | ACTAGCAAAN | 660 |
| | AAGTG | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTNTTTTT | TTTTTTTGC | AGGAAGGATT | CCATTTATTG | TGGATGCATT | TTCACAATAT | 60 |
| ATGTTTATTG | GAGCGATCCA | TTATCAGTGA | AAAGTATCAA | GTGTTTATAA | NATTTTAGG | 120 |
| AAGGCAGATT | CACAGAACAT | GCTNGTCNGC | TTGCAGTTT | ACCTCGTANA | GATNACAGAC | 180 |
| AATTATAGTC | NAACCGATAA | ACNAGGAATT | TACTTTTCAA | AAGATTAAT | CCAAACTGAA | 240 |
| CAAAATTCTA | CCCTGAAACT | TACTCCATCC | AAATATTGGA | ATAANAGTCA | GCAGTGATAC | 300 |
| ATTCTCTCT | GAACTTTAGA | TTTTCTAGAA | AAATATGTAA | TAGTGATCAG | GAAGAGCTCT | 360 |
| TGTCAAAAG | TACAACNAAG | CAATGTTCCC | TTACCATAGG | CCTTAATTCA | AACTTTGATC | 420 |
| CATTCACTC | CCATCACGGG | AGTCAATGCT | ACCTGGGACA | CTTGTATTT | GTTCATNCTG | 480 |
| ANCNNTGGCTT | AA | | | | | 492 |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| TTTNTTTTGN | ATTCANTCT | GTANNAANTA | TTTCATTAT | GTTTATTANA | AAAATATNAA | 60 |
| TGTNTCCACN | ACAAATCATN | TTACINTNAGT | AAGAGGCCAN | CTACATTGTA | CAACATACAC | 120 |
| TGAGTATATT | TTGAAAAGGA | CAAGTTTAAA | GTANACNCAT | ATTGCCGANC | ATANCACATT | 180 |
| TATACATGGC | TTGATTGATA | TTTAGCACAG | CANAAACTGA | GTGAGTTACC | AGAAAANAAAT | 240 |
| NATATATGTC | AATCNGATTT | AAGATACAAA | ACAGATCCTA | TGGTACATAN | CATCNTGTAG | 300 |
| GAGTTGTGGC | TTTATGTTA | CTGAAAGTCA | ATGCAGTTCC | TGTACAAAGA | GATGGCCGTA | 360 |
| AGCATTCTAG | TACCTCTACT | CCATGGTTAA | GAATCGTACA | CTTATGTTA | CATATGTNCA | 420 |
| GGGTAAGAAT | TGTGTTAAGT | NAANTTATGG | AGAGGTCCAN | GAGAAAATT | TGATNCAA | 478 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTCTAG | TTTCCTCTAC | GGATGAGAGA | CTGGCTCAAG | AATATCCTCA | TGCACTTTA | 240 |
| TGAAGCCNAC | TCTGAACACG | CTGGTTATCT | NAGATGAGAA | NCAGAGAAAT | AAAGTCNAGA | 300 |
| AAATTTACCT | GGANGAAAAG | AGGCTTNNGG | CTGGGGACCA | TCCCATTGAA | CCTTCTCTTA | 360 |
| ANGGACTTTA | AGAANAAAAT | ACCACATGTN | TGTNGTATCC | TGGTGCNNGG | CCGTTTANTG | 420 |
| AACNTNGACN | NCACCCTTNT | GGAATANANT | CTTGACNGCN | TCCTGAACCTT | GCTCCTCTGC | 480 |
| GA | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60 |
| CGACTGCGAC | GACGGCGCG | GCGACAGTCG | CAGGTGCAGC | GCGGGCCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCGCA | GAGGTCTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCGGT | GAANGCGGGA | GGCCTCGGGG | AGCCCTCGG | GAAGGGCGGC | 240 |
| CCGAGAGATA | CGCAGGTGCA | GGTGGCCGCC | | | | 270 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTGGAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTTGCA | 60 |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTCA | GTCAACTTCC | TTTGTCTGTGG | 120 |
| TTGATTGGTT | TGTCTTATG | GGGGCGGGGT | GGGGTAGGGG | AAANGAAGC | ANAANTAAACA | 180 |
| TGGAGTGGGT | GCACCCCTCCC | TGTAGAACCT | GGTTACNAAA | GCTTGGGGCA | GTTCACCTGG | 240 |
| TCTGTGACCG | TCATTTTCTT | GACATCAATG | TTATTAGAAG | TCAGGATATC | TTTTAGAGAG | 300 |
| TCCAATGTNT | CTGGAGGGAG | ATTAGGGTTT | CTTGCCAANA | TCCAANAAA | ATCCACNTGA | 360 |
| AAAAGTTGGA | TGATNCANGT | ACNGAATACC | GANGGCATAN | TTCTCATANT | CGGTGGCCA | 419 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| TGGCACTTAA | TCCATTTTA | TTTCAAAATG | TCTACAAANT | TTNAATNCNC | CATTATAACNG | 120 |
| GTNATTTTNC | AAAATCTAAA | NNTTATTCAA | ATNTNAGCCA | AANTCCTTAC | NCAAATNNAA | 180 |
| TACNCNCAAA | AATCAAAAAT | ATACNTNTCT | TTCAGCAAAC | TTNGTTACAT | AAATTAAAAAA | 240 |
| AATATATACG | GCTGGTGT | TCAAAGTACA | ATTATCTAA | CACTGCAAAC | ATNTTTNNAA | 300 |
| GGAACAAAAA | TAAAAAA | CACTNCCGCA | AAGGTAAAG | GGAACAAACAA | ATTCTNTTTA | 360 |
| CAACANCNNC | NATTATAAAA | ATCATATCTC | AAATCTTAGG | GGAATATATA | CTTCACACNG | 420 |
| GGATCTAAC | TTTTACTNCA | CTTGTGTTAT | TTTTTANAA | CCATTGTNTT | GGGCCAACA | 480 |
| CAATGGNAAT | NCCNCCNCCN | TGGACTAGT | | | | 509 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTG | CCCCCCTCTT | ATAAAAAACA | AGTACCATT | TTATTTTACT | 60 |
| TACACATATT | TATTTTATAA | TTGGTATTAG | ATATTCAAAA | GGCAGCTTT | AAAATCAAAC | 120 |
| TAAATGGAAA | CTGCCCTAGA | TACATAATT | TTAGGAATT | GCTTAAAATC | TGCCCTAAAGT | 180 |
| GAAAATCTTC | TCTAGCTCTT | TTGACTGTAA | ATTTTGACT | CTTGTAAAAC | ATCCAAATT | 240 |
| ATTTTTCTTG | TCTTTAAAAT | TATCTAATCT | TTCCATT | TCCCTATTCC | AAGTCAATT | 300 |
| GCTTCTCTAG | CCTCAATTCC | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT | TTTCCTAAA | 360 |
| AGGGAAAACA | GGAAGAGANA | ATGGCACACA | AAACAAACAT | TTTATATTCA | TATTCTACC | 420 |
| TACGTTAATA | AAATAGCATT | TTGTAAGCC | AGCTCAAAAG | AAGGCTTAGA | TCCTTTATG | 480 |
| TCCATT | TTAG | TCACTAAACG | ATATCNAAG | TGCCAGAATG | CAAAGGTTT | 540 |
| ATTCAAAAGC | TAATATAAGA | TATTCACAT | ACTCATCTT | GTGAACATTT | | 583 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|-----|
| TTTTTTTTNT | TTTTTTTTTT | TTTTTNCTC | TTCTTTTTTT | TTGANAATGA | GGATCGAGTT | 60 |
| TTTCACTCTC | TAGATAGGGC | ATGAAGAAAA | CTCATTTTC | CAGCTTTAAA | ATAACAATCA | 120 |
| AATCTCTTAT | GCTATATCAT | ATTTAAGTT | AAACTAATGA | GTCACTGGCT | TATCTTCTCC | 180 |
| TGAAGGAAAT | CTGTTCATTC | TTCTCATTCA | TATAGTTATA | TCAAGTACTA | CCTTGATAT | 240 |
| TGAGAGGTTT | TTCTTCTCTA | TTTACACATA | TATTCCATG | TGAATTGTA | TCAAACCTTT | 300 |
| ATTTTCATGC | AAACTAGAAA | ATAATGTNTT | CTTTGCATA | AGAGAAGAGA | ACAATATNAG | 360 |
| CATTACAAAA | CTGCTCAAAT | TGTTGTTAA | GNTTATCCAT | TATAATTAGT | TNGGCAGGAG | 420 |
| CTAATACAAA | TCACATTAC | NGACNAGCAA | TAATAAAACT | GAAGTACCAAG | TTAAATATCC | 480 |
| AAAATAATT | AAGGAACATT | TTTAGCCTGG | GTATAATTAG | CTAATTCACT | TTACAAGCAT | 540 |
| TTATTNAGAA | TGAATTACA | TGTTATTATT | CCNTAGCCCCA | ACACAATGG | | 589 |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | | | | | | | |
|-------------|------------|------------|------------|------------|----------|-------|-----|
| TTTTNTTTT | TTTTTCAGT | AATAATCAGA | ACAATATT | TTTTATATT | AAAATT | CAT | 60 |
| AGAAAAGTGC | CTTACATTTA | ATAAAAGTT | GTTTCTCAA | GTGATCAGAG | GAATT | AGATA | 120 |
| TNGTCTTGAA | CACCAATATT | AATTTGAGGA | AAATACACCA | AAATACATTA | AGTAAATT | TAT | 180 |
| TTAAGATCAT | AGAGCTTGTA | AGTAAAAGA | TAAAATTG | CCTCAGAAAC | TCTGAGC | CATT | 240 |
| AAAAAATCCAC | TATTAGCAA | AAATTACTA | TGGACTT | GCTTAA | TGTGAT | GAAT | 300 |
| ATGGGGTGT | ACTGGTAAAC | CAACACATTC | TGAAGGATAC | ATTACTTAGT | GATAGATT | CCT | 360 |
| TATGTACTTT | GCTANATNAC | GTGGATATGA | GTTGACAAGT | TTCTCTT | TCAATCTT | TTT | 420 |
| AAGGGGCNGA | NGAAATGAGG | AAGAAAAGAA | AAGGATTACG | CATACTGTTC | TTTCTAT | NGG | 480 |
| AAGGATTAGA | TATGTTCC | TTGCCAATAT | AAAAAAATA | ATAATGTT | CTACTAGT | GAA | 540 |
| AACCC | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | | | | | | | |
|-------------|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTTT | TTTTTAGTC | AAGTTCTNA | TTTTTATT | AATTAAAGTC | TTGGTCATT | TT | 60 |
| CATTTATTAG | CTCTGCACT | TACATATT | AATTAAAGAA | ACGTINTT | ACAACTGTNA | ACAA | 120 |
| CAATTTATAA | ATGTAAGGTG | CCATTATTGA | GTANATAT | TCCTCCAAGA | GTGGATGTGT | GTGGATGTGT | 180 |
| CCCTTCTCCC | ACCAACTAAT | GAANCAGCAA | CATTAGTTA | ATTTTATTAG | TAGATNATAC | TAGATNATAC | 240 |
| ACTGCTGCAA | ACGCTAATT | TCTTCTCCAT | CCCCATGTNG | ATATTGTGT | TATGTGTGAG | TATGTGTGAG | 300 |
| TTGGTNAGAA | TGCATCANCA | ATCTNACAAT | CAACAGCAAG | ATGAAGCTAG | GCNTGGGCTT | GCNTGGGCTT | 360 |
| TCGGTGAAA | TAGACTGTGT | CTGTCGAAT | CAAATGATCT | GACCTATCCT | CGGTGGCAAG | CGGTGGCAAG | 420 |
| AACTCTTCGA | ACCGCTTC | CAAAGGCNGC | TGCCACATT | GTGGCNTCTN | TTGCACTTGT | TTGCACTTGT | 480 |
| TTCAAAA | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-----|
| TGAATTGGCT | AAAAGACTGC | ATTTTANAA | CTAGCAACTC | TTATTCTTT | CCTTTAAAAA | AA | 60 |
| TACATAGCAT | TAAATCCAA | ATCCTATT | AAGACCTGAC | AGCTTGAGAA | GGTCACTACT | GGTCACTACT | 120 |
| GCATTTATAG | GACCTCTGG | TGGTTCTGCT | GTTACNTT | AANTCTGACA | ATCCTTGANA | ATCCTTGANA | 180 |
| ATCTTTCGAT | GCAGAGGAGG | TAAAAGGTAT | TGGATTTC | CAGAGGAANA | ACACAGCGCA | ACACAGCGCA | 240 |
| GAAATGAAGG | GGCCAGGCTT | ACTGAGCTG | TCCACTGGAG | GGCTCATGGG | TGGGACATGG | TGGGACATGG | 300 |
| AAAAGAAGGC | AGCCTAGGCC | CTGGGGAGCC | CA | | | | 332 |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | | | | | | |
|------------|-------------|--------------|------------|-------------|------------|-----|
| AGGGCGTGGT | GCGGAGGGCG | TTACTGTTTT | GTCTCAGTAA | CAATAAATAC | AAAAAGACTG | 60 |
| GTGTTGTTCC | GGCCCCATCC | AACCAACGAAG | TTGATTTCTC | TTGTGTGCGAG | AGTGACTGAT | 120 |
| TTAAAGGAC | ATGGAGCTTG | TCACAATGTC | ACAATGTCAC | AGTGTGAAGG | GCACACTCAC | 180 |
| TCCCGCGTGA | TTCACATTTA | GCAACCAACA | ATAGCTCATG | AGTCCATACT | TGTAAATACT | 240 |
| TTTGGCAGAA | TACTTNTGA | AACTTGCGAGA | TGATAACTAA | GATCCAAGAT | ATTTCCCAAA | 300 |
| GTAAATAGAA | GTGGGTCTATA | ATATTAAATTAA | CCTGTTACAA | TCAGCTTCCA | TTTACAAGTC | 360 |
| ATGAGCCCAG | ACACTGACAT | CAAACATAAGC | CCACTTAGAC | TCCTCACCAAC | CAGTCTGTCC | 420 |
| TGTCATCAGA | CAGGAGGCTG | TCACCTTGAC | CAAATTCTCA | CCAGTCAATC | ATCTATCCAA | 480 |
| AAACCATTAC | CTGATCCACT | TCCGGTAATG | CACCACCTTG | GTGA | | 524 |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGGTGAGGAA | ATCCAGAGTT | GCCATGGAGA | AAATTCCAGT | GTCAGCATTC | TTGCTCCTTG | 60 |
| TGGCCCTCTC | CTACACTCTG | GCCAGAGATA | CCACAGTCAA | ACCTGGAGCC | AAAAAGGACA | 120 |
| CAAAGGACTC | TCGACCCAAA | CTGCCCCAGA | CCCTCTCCA | | | 159 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| ACTCCCTGGC | AGACAAAGGC | AGAGGGAGAGA | GCTCTGTTAG | TTCTGTGTTG | TTGAAC TGCC | 60 |
| ACTGAATTTC | TTTCCACTTG | GACTATTACA | TGCCANTTGA | GGGACTAATG | AAAAAACGTA | 120 |
| TGGGGAGATT | TTANCCAATT | TANGTNTGTA | AATGGGGAGA | CTGGGGCAGG | CGGGAGAGAT | 180 |
| TTGCAGGGTG | NAAATGGGAN | GGCTGGTTG | TTANATGAAC | AGGGACATAG | GAGGTAGGCA | 240 |
| CCAGGATGCT | AAATCA | | | | | 256 |

(2) INFORMATION FOR SEQ ID NO:211:

130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACATTGTTTT | TTTGAGATAA | AGCATTGAGA | GAGCTCTCCT | TAACGTGACA | CAATGGAAGG | 60 |
| ACTGGAACAC | ATACCCACAT | CTTTGTTCTG | AGGGATAATT | TTCTGATAAA | GTCTTGCTGT | 120 |
| ATATTCAAGC | ACATATGTTA | TATATTATTC | AGTTCCATGT | TTATAGCCTA | GTAAAGGAGA | 180 |
| GGGGAGATAC | ATTCNGAAAG | AGGACTGAAA | GAAATACTCA | AGTNGAAAAA | CAGAAAAAGA | 240 |
| AAAAAAGGAG | CAAATGAGAA | GCCT | | | | 264 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ACCCAAAAAT | CCAATGCTGA | ATATTTGGCT | TCATTATTCC | CANATTCTTT | GATTGTCAAA | 60 |
| GGATTTAATG | TTGTCTCAGC | TTGGGCACTT | CAGTTAGGAC | CTAAGGATGC | CAGCCGGCAG | 120 |
| GTTTATATAT | GCAGCAACAA | TATTCAAGCG | CGACAACAGG | TTATTGAACT | TGCCCAGCAG | 180 |
| TTNAATTTC | TTCCCATTGA | CTTGGGATCC | TTATCATCAG | CCAGAGAGAT | TGAAAATTAA | 240 |
| CCCCTACNAC | TCTTTACTCT | CTGGANAGGG | CCAGTGGTGG | TAGCTATAAG | CTTGGCCACA | 300 |
| TTTTTTTTTC | CTTTATTCCCT | TTGTCAGA | | | | 328 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTATGAGC | AGAGCGACAT | ATCCNAGTGT | AGACTGAATA | AAACTGAATT | CTCTCCAGTT | 60 |
| TAAAGCATTG | CTCACTGAAG | GGATAGAAGT | GACTGCCAGG | AGGGAAAGTA | AGCCAAGGCT | 120 |
| CATTATGCCA | AAGGANATAT | ACATTTCAAT | TCTCCAAACT | TCTTCCTCAT | TCCAAGAGTT | 180 |
| TTCAATATTT | GCATGAACCT | GCTGATAANC | CATGTTAANA | AACAAATATC | TCTCTNACCT | 240 |
| TCTCATCGGT | | | | | | 250 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ACCCAGAAC | CAATGCTGAA | TATTTGGCTT | CATTATTCCC | AGATTCTTG | ATTGTCAAAG | 60 |
| GATTTAATGT | TGTCTCAGCT | TGGGCACCTC | AGTTAGGACC | TAAGGATGCC | AGCCGGCAGG | 120 |
| TTTATATATG | CAGCAACAAT | ATTCAAGCGC | GACAACAGGT | TATTGAACTT | GCCCCGCCAGT | 180 |
| TGAATTTCAT | TCCCATTGAC | TTGGGATCCT | TATCATCAGC | CANAGAGATT | GAAAATTAC | 240 |
| CCCTACGACT | CTTTACTCTC | TGGAGAGGGC | CAGTGGTGGT | AGCTATAAGC | TTGGCCACAT | 300 |
| TTTTTTTCC | TTTATTCCTT | TGTCAGAGAT | GCGATTATC | CATATGCTAN | AAACCAACAG | 360 |
| AGTGACTTTT | ACAAAATTCC | TATAGANATT | GTGAATAAAA | CCTTACCTAT | AGTTGCCATT | 420 |
| ACTTTGCTCT | CCCTAATATA | CCTC | | | | 444 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTATGAGC | AGAGCGACAT | ATCCAAGTGT | ANACTGAATA | AAACTGAATT | CTCTCCAGTT | 60 |
| TAAAGCATTG | CTCACTGAAG | GGATAGAAGT | GACTGCCAGG | AGGGAAAGTA | AGCCAAGGCT | 120 |
| CATTATGCCA | AAGGANATAT | ACATTTCAAT | TCTCCAAACT | TCTTCCTCAT | TCCAAGAGTT | 180 |
| TTCAATATTG | GCATGAACCT | GCTGATAAGC | CATGTTGAGA | AACAAATATC | TCTCTGACCT | 240 |
| TCTCATCGGT | AAGCAGAGGC | TGTAGGCAAC | ATGGACCATA | GCGAANAAAA | AACTTAGTAA | 300 |
| TCCAAGCTGT | TTTCTACACT | GTAACCAGGT | TTCCAACCAA | GGTGAAATC | TCCTATACTT | 360 |
| GGTGCC | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTATAAAC | AGAACTCCAC | TGCANGAGGG | AGGGCCGGGC | CAGGAGAAC | TCCGCTTGTC | 60 |
| CAAGACAGGG | GCCTAAGGAG | GGTCTCCACA | CTGCTNNTAA | GGGCTNTTNC | ATTTTTTTAT | 120 |
| TAATAAAAAG | TNAAAAGGC | CTCTTCTCAA | CTTTTTTCCC | TTNGGCTGGA | AAATTTAAAA | 180 |
| ATCAAAAATT | TCCTNAAGTT | NTCAAGCTAT | CATATATACT | NTATCCTGAA | AAAGCAACAT | 240 |

AATTCTTCCT TCCCTCCCTT

260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTAN AAATGTTATA ATTTCAGGAA NAGGAACGCA TATAATTGTA
 TCTTGCCTAT AATTTCTAT TTTAATAAGG AAATAGCAA TTGGGGTGGG GGGAAATGTAG
 GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAAATTTT
 ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCCTA
 ATATCCTTCA TGCTTGTAAA GT

60
 120
 180
 240
 262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCAA CCCCTGAGCA
 CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC
 AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA
 ANAAATCAGC AGACACAGGT GTAAA

60
 120
 180
 205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA
 ACCACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA

60
 114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | |
|---|----|
| ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA | 60 |
| AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT | 93 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | |
|--|-----|
| ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGA TTCCATGAGG | 60 |
| TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC | 120 |
| CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT | 167 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | |
|---|-----|
| AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC | 60 |
| GTTCTTCACC TGTCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA | 120 |
| ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA | 180 |
| TTTCTCTT TATATTTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAATCTTT | 240 |
| TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT | 300 |
| CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T | 351 |

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | |
|---|-----|
| AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG GGACTGATAT | 60 |
| TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTC CTTACATTGT CTTGACAAGA | 120 |
| TTAAATGTC TGTGCCAAA TTTTGTATTT TATTTGGAGA CTTCCTATCA AAAGTAATGC | 180 |
| TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT | 240 |
| TAAAAGATTT TGATTCCTG GAATGACAAT TATATTTAA CTTTGGGGGG GGAAANAGTT | 300 |
| ATAGGACAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG | 360 |
| ACCATTAAGC TATATGTTA AAA | 383 |

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

| | |
|--|-----|
| CCCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA | 60 |
| AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT | 120 |
| GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA | 180 |
| GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC | 240 |
| AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT | 300 |
| TTTARACTCM GCATTGTGAC | 320 |

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;

(b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| | | | |
|---|--|---|---|
| (51) International Patent Classification 6 : G01N 33/574, 33/577, C07K 16/30, A61K 39/395, 47/48, C12Q 1/68, G01N 33/543 | | A3 | (11) International Publication Number: WO 98/37418 (43) International Publication Date: 27 August 1998 (27.08.98) |
| (21) International Application Number: PCT/US98/03690 | | (81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). | |
| (22) International Filing Date: 25 February 1998 (25.02.98) | | | |
| (30) Priority Data: 08/806,596 25 February 1997 (25.02.97) US 08/904,809 1 August 1997 (01.08.97) US 09/020,747 9 February 1998 (09.02.98) US | | | |
| (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). | | Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> | |
| (72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). | | (88) Date of publication of the international search report: 25 February 1999 (25.02.99) | |
| (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). | | | |

(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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INTERNATIONAL SEARCH REPORT

International Application No
PC., US 98/03690A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 G01N33/574 G01N33/577 G01N33/543 C07K16/30 C12Q1/68
A61K39/395 A61K47/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12Q C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ¹ | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------------------|--|-----------------------|
| A | WO 96 21671 A (UNIV COLUMBIA ;FISHER PAUL B (US); SHEN RUOQUIAN (US)) 18 July 1996 see the whole document --- | 1-10, 12-22 |
| A | EL-SHIRBINY A M: "PROSTATIC SPECIFIC ANTIGEN" ADVANCES IN CLINICAL CHEMISTRY, vol. 31, 1994, pages 99-133, XP000617158 see the whole document --- | 1-10, 12-22 |
| A | WO 93 14775 A (WRIGHT GEORGE L JR) 5 August 1993 see the whole document --- | 1-10, 12-22 -/- |

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

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Date of the actual completion of the international search

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Date of mailing of the international search report

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Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No
PCT/JS 98/03690

| C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT | | |
|---|--|-----------------------|
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| A | WO 94 09820 A (SLOAN KETTERING INST CANCER ;ISRAELI RON S (US); HESTON WARREN D W) 11 May 1994 see the whole document --- | 1-10, 12-22 |
| A | WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document --- | 1-10, 12-22 |
| A | ROBSON C N ET AL: "IDENTIFICATION OF PROSTATIC ANDROGEN REGULATED GENES USING THE DIFFERENTIAL DISPLAY TECHNIQUE" PROCEEDINGS OF THE ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, TORONTO, MAR. 18 - 22, 1995, no. MEETING 86, 18 March 1995, AMERICAN ASSOCIATION FOR CANCER RESEARCH, page 266 XP002019344 see the whole document --- | 1-10, 12-22 |
| A | BLOK L J ET AL: "ISOLATION OF CDNAS THAT ARE DIFFERENTIALLY EXPRESSED BETWEEN ANDROGEN-DEPENDENT AND ANDROGEN-INDEPENDENT PROSTATE CARCINOMA CELLS USING DIFFERENTIAL DISPLAY PCR" PROSTATE, vol. 26, no. 4, April 1995, pages 213-224, XP000611577 see the whole document --- | 1-10, 12-22 |
| A | ALEXEYEV ET AL.: "IMPROVED ANTIBIOTIC-RESISTANCE GENE CASSETTES AND OMEGA ELEMENTS FOR E.COLI VECTOR CONSTRUCTION AND IN VITRO DELETION/INSERTION MUTAGENESIS" GENE, vol. 160, 1995, pages 63-67, XP002076033 & DATABASE EMBL AC: U35129, 1995 "pBSL141" see abstract --- | 1-10, 12-22 |
| P,A | DATABASE EMBL AC: AA453562, 11 June 1997 HILLIER ET AL.: "HOMO SAPIENS cDNA CLONE 788180" XP002075910 see abstract ----- | 1-10, 12-22 |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/03690

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 6 and 7 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-10, 12-22 (all partially)

Remark on Protest

The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-10,12-22 (all partially)

Invention 1:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 2 or oligonucleotide primers specific for a DNA molecule with Seq. ID 2 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 2 used in a method for inhibiting development of prostate cancer.

2. Claims: 1-10,12-22 (all partially)

Inventions 2-130:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 3 or oligonucleotide primers specific for a DNA molecule with Seq. ID 3 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 3 used in a method for inhibiting development of prostate cancer.

...ibidem for Seq. ID 8-29,
41-45,47-52,54-65,70,73,74,79,81,87,90,92,93,97,103,104,107,1
15-160,171,181,188,191,193,194,198,203,204,207,209-211,220,22
2-224.

3. Claims: 1-4,8,9,11-22 (all partially)

Inventions 131-215:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 5 or oligonucleotide primers specific for a DNA molecule with Seq. ID 5 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 5 used in a method for inhibiting development of prostate cancer.

...ibidem for each of Seq. ID
6,7,30-40,46,53,66-69,71,72,75-78,80,82-86,88,89,91,94-96,98-
102,105,106,161-170,179,180,182-187,189,190,192,195-197,198-2
02,205,206,208,212-219.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/03690

| Patent document cited in search report | Publication date | Patent family member(s) | | Publication date |
|--|------------------|-------------------------|---|------------------|
| WO 9621671 | A 18-07-1996 | AU 4751196 | A | 31-07-1996 |
| | | CA 2209941 | A | 18-07-1996 |
| | | EP 0804458 | A | 05-11-1997 |
| WO 9314775 | A 05-08-1993 | CA 2106487 | A | 01-08-1993 |
| WO 9409820 | A 11-05-1994 | CA 2147499 | A | 11-05-1994 |
| | | EP 0668777 | A | 30-08-1995 |
| | | JP 8506005 | T | 02-07-1996 |
| | | US 5538866 | A | 23-07-1996 |
| WO 9504548 | A 16-02-1995 | AU 686660 | B | 12-02-1998 |
| | | AU 7631294 | A | 28-02-1995 |
| | | CA 2168952 | A | 16-02-1995 |
| | | EP 0721345 | A | 17-07-1996 |
| | | JP 9504000 | T | 22-04-1997 |